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MPSRCH (TM)

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Release 3.1A John F. Collins, Biocomputing Research Unit.

MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Mon Aug 2 11:36:56 1999; MasPar time 104.45 Seconds
716.503 Million cell updates/sec

Tabular output not generated.

Title: >US-09-121-239-23
Description: (1-27) from US09121239.seq
Perfect Score: 27
N.A. Sequence: 1 UCUGACUUUGAGCCUCAGGGUCUGAGU 27
Comp: AGACTGAAACTCGGAGTCCCAGACTCA

Scoring table: TABLE default
Gap 10

Nmatch STD : Dbase 0; Query 0

Searched: 646147 seqs, 1385953633 bases x 2

Post-processing: Minimum Match 0%
Listing first 1000 summaries
Maximum DB seq length 50

Database: embl58
1:em_ba1 2:em_ba2 3:em_fun 4:em_htg 5:em_hum1 6:em_hum2
7:em_in 8:em_om 9:em_or 10:em_ov 11:em_pat 12:em_ph
13:em_pl 14:em_ro 15:em_sts 16:em_vi

Database: genbank111
17:gb_ba1 18:gb_ba2 19:gb_htg1 20:gb_htg2 21:gb_in1
22:gb_in2 23:gb_om 24:gb_ov 25:gb_pat 26:gb_ph 27:gb_pl1
28:gb_pl2 29:gb_pr1 30:gb_pr2 31:gb_pr3 32:gb_ro
33:gb_st 34:gb_sts 35:gb_sy 36:gb_un 37:gb_vi

Statistics: Mean 7.012; Variance 3.374; scale 2.078

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length DB	ID	Description	Pred. No.
c 1	22	81.5	22 25	I92877	Sequence 1 from patent	3.08e-02
c 2	22	81.5	22 25	I44731	Sequence 10 from paten	3.08e-02
3	15	55.6	16 11	E13680	Substrate os minizyme.	4.29e+02
c 4	15	55.6	20 25	I23911	Sequence 13 from paten	4.29e+02

Note: Post-processor removed 996 summaries from list due to search parameters chosen.

ALIGNMENTS

RESULT 1
LOCUS I92877 22 bp DNA PAT 17-JUL-1998
DEFINITION Sequence 1 from patent US 5728822.
ACCESSION I92877
NID g3937347
VERSION I92877.1 GI:3937347
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 22)
AUTHORS Macfarlane,D.E.
TITLE Quaternary amine surfactants and methods of using same in isolation of RNA
JOURNAL Patent: US 5728822-A 1 17-MAR-1998;
FEATURES Location/Qualifiers
source 1..22
/organism="unknown"
BASE COUNT 6 a 7 c 5 g 4 t
ORIGIN

Query Match 81.5%; Score 22; DB 25; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.08e-02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 TCAGACCCTGAGGCTCAAAGTC 22
||||||||||||||||||||||
Cp 25 TCAGACCCTGAGGCTCAAAGTC 4

RESULT 2
LOCUS I44731 22 bp DNA PAT 22-JUL-1997
DEFINITION Sequence 10 from patent US 5635385.
ACCESSION I44731
NID g2469444
VERSION I44731.1 GI:2469444
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 22)
AUTHORS Leopold,P.H., Shore,S.K., Reddy,M.V.R. and Reddy,E.Premkumar
TITLE Multi-unit ribozyme inhibition of oncogene gene expression
JOURNAL Patent: US 5635385-A 10 03-JUN-1997;
FEATURES Location/Qualifiers
source 1..22
/organism="unknown"
BASE COUNT 6 a 7 c 5 g 4 t
ORIGIN

Query Match 81.5%; Score 22; DB 25; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.08e-02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 TCAGACCCTGAGGCTCAAAGTC 22
||||||||||||||||||||||
Cp 25 TCAGACCCTGAGGCTCAAAGTC 4

RESULT 3
ID E13680 standard; RNA; UNC; 16 BP.
AC E13680;
SV E13680.1
NI d1201477
DT 23-JUN-1998 (Rel. 56, Created)
DT 23-JUN-1998 (Rel. 56, Last updated, Version 1)
DE Substrate os minizyme.
KW JP 1997224673-A/8.
OS unidentified
OC unclassified.
RN [1]
RP 1-16
RA Tahira K., Nishikawa S., Yamada A., Hanada K.;
RT "PAIR OF MINIRIBOZYME, MINIRIBOZYME-DIMER, CUTTING-DEACTIVATION OF
RT TARGET RNA BY THEM AND MEDICINE";

RL Patent number JP 1997224673-A/8, 02-SEP-1997.
RL AGENCY OF IND SCIENCE & TECHNOL, HITACHI CHEM CO LTD, TAISHO PHARMACEUT
RL CO LTD.
CC OS None
CC OC Artificial sequences.
CC PN JP 1997224673-A/8
CC PD 02-SEP-1997
CC PF 22-FEB-1996 JP 1996034898
CC PI TAHIRA KAZUMASA, NISHIKAWA SATOSHI, YAMADA AKIRA,
CC PI HANADA KAZUNORI
CC PC C12N15/09,A61K48/00,A61K48/00,A61K48/00,A61K49/00,C07H21/02,
CC PC C07H21/04,
CC PC C12N9/16,C12Q1/68//A01N63/00;
CC CC strandedness: Single;
CC CC topology: Linear;
CC CC hypothetical: No;
CC FH Key Location/Qualifiers
CC FH
CC FT source 1. .16
CC FT /organism="Artificial sequences"
FH Key Location/Qualifiers
FH
FT source 1. .16
FT /organism="unidentified"
FT /db_xref="taxon:32644"
SQ Sequence 16 BP; 2 A; 4 C; 6 G; 4 T; 0 other;

Query Match 55.6%; Score 15; DB 11; Length 16;
Best Local Similarity 73.3%; Pred. No. 4.29e+02;
Matches 11; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 1 CCTCAGGGTCTGAGT 15
|:|||||:|:|||:
Qy 13 CCUCAGGGUCUGAGU 27

RESULT 4
LOCUS I23911 20 bp DNA PAT 21-NOV-1996
DEFINITION Sequence 13 from patent US 5541060.
ACCESSION I23911
NID g1603781
VERSION I23911.1 GI:1603781
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bell,G.I., Stoffel,M., Takeda,J., Vionnet,N., Yasuda,K.,
Pilkis,S.J., Zouali,H., Velho,G., Cohen,D. and Froguel,P.
TITLE Detection of glucokinase-linked early-onset non-insulin-dependent
diabetes mellitus
JOURNAL Patent: US 5541060-A 13 30-JUL-1996;
FEATURES Location/Qualifiers
source 1. .20
/organism="unknown"
BASE COUNT 6 a 5 c 4 g 5 t
ORIGIN

Query Match 55.6%; Score 15; DB 25; Length 20;
Best Local Similarity 89.5%; Pred. No. 4.29e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 1 TCAGATTCTGAGGCTCAAA 19
||||| ||||||||||||
Cp 25 TCAGACCCTGAGGCTCAAA 7

Search completed: Mon Aug 2 11:45:05 1999
Job time : 489 secs.

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MPSRCH (TM)

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Release 3.1A John F. Collins, Biocomputing Research Unit.

MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Mon Aug 2 11:56:31 1999; MasPar time 25.66 Seconds
225.494 Million cell updates/sec

Tabular output not generated.

Title: >US-09-121-239-23
Description: (1-27) from US09121239.seq
Perfect Score: 27
N.A. Sequence: 1 UCUGACUUUGAGCCUCAGGGUCUGAGU 27
Comp: AGACTGAAACTCGGAGTCCCAGACTCA

Scoring table: TABLE default
Gap 10

Nmatch STD : Dbase 0; Query 0

Searched: 271905 seqs, 107135622 bases x 2

Post-processing: Minimum Match 0%
Listing first 1000 summaries
Maximum DB seq length 50

Database: n-geneseq35
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33
34:part34 35:part35 36:part36 37:part37 38:part38
39:part39 40:part40 41:part41 42:part42 43:part43
44:part44 45:part45 46:part46 47:part47 48:part48
49:part49 50:part50 51:part51 52:part52 53:part53
54:part54 55:part55 56:part56 57:part57 58:part58
59:part59 60:part60

Statistics: Mean 5.548; Variance 3.416; scale 1.624

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
c	1	24	88.9	50	51	V66349	CML-2 chromosomal tra	1.07e-03
c	2	24	88.9	50	19	T15571	CML-2 chromosomal tra	1.07e-03
c	3	24	88.9	50	28	T42417	CML chromosomal trans	1.07e-03
c	4	24	88.9	50	15	Q86626	CML chromosomal trans	1.07e-03
c	5	22	81.5	22	3	Q14244	Primer CMLII.	1.41e-02
c	6	22	81.5	22	10	Q62302	PCR primer for amplif	1.41e-02
c	7	22	81.5	22	36	T88787	Leukaemic cell BCR-AB	1.41e-02
c	8	20	74.1	50	40	V01841	PCR primer abl50 used	1.73e-01
	9	19	70.4	24	50	V58784	Detection probe for B	5.98e-01
c	10	17	63.0	23	15	Q86124	bcr-abl mRNA junction	6.51e+00
c	11	17	63.0	27	28	T62502	Murine retrovirus con	5.51e+00
	12	16	59.3	27	28	T62502	Murine retrovirus con	2.08e+01
	13	15	55.6	16	35	T91968	RNA sequence disclose	6.46e+01
c	14	15	55.6	20	9	Q51057	Human glucokinase exo	6.46e+01
c	15	15	55.6	20	45	V39479	Chronic myelogenous/a	6.46e+01
	16	15	55.6	40	45	V39474	Chronic myelogenous l	6.46e+01
	17	15	55.6	40	45	V39473	Acute lymphocytic leu	6.46e+01
c	18	15	55.6	48	10	Q56492	PCR primer for K562 c	6.46e+01
c	19	14	51.9	29	29	T38971	Interleukin IL-3 3' P	1.94e+02
c	20	13	48.1	21	3	Q08506	Sequence of 3' probe,	5.64e+02
c	21	13	48.1	21	2	Q10345	Probe to the human in	5.64e+02
c	22	13	48.1	21	7	Q42804	Human IL-3 probe.	5.64e+02
	23	13	48.1	22	29	T63590	CD59 PCR primer used	5.64e+02
	24	13	48.1	24	46	V42514	PCR primer used to am	5.64e+02
c	25	13	48.1	27	54	V95538	Human c-fos hammerhea	5.64e+02
c	26	13	48.1	29	5	Q28596	HLA DPA1 primer #513.	5.64e+02
c	27	13	48.1	33	31	T47213	PCR primer for plasmi	5.64e+02
	28	13	48.1	42	36	T70502	Human Immunoglobulin	5.64e+02
	29	13	48.1	42	3	Q23427	Probe for human D seg	5.64e+02
	30	13	48.1	42	39	V12519	Probe DXP4 for human	5.64e+02
	31	13	48.1	42	50	V38133	Oligonucleotide DXP4	5.64e+02
	32	13	48.1	42	28	T37221	Human antibody D segm	5.64e+02
	33	13	48.1	42	7	Q44165	Probe DXP4 to isolate	5.64e+02
	34	13	48.1	42	34	T73451	Human D segment genom	5.64e+02
	35	13	48.1	45	28	T51509	Fragment of cDNA enco	5.64e+02
	36	13	48.1	45	43	V30882	Human p53UBC hybridis	5.64e+02
c	37	12	44.4	22	52	V51543	Zea mays genome forwa	1.57e+03
c	38	12	44.4	24	40	V12138	Synthetic Sus scrofa	1.57e+03
c	39	12	44.4	27	59	V98214	Human EGF-R hammerhea	1.57e+03
c	40	12	44.4	27	59	V98051	Human EGF-R hammerhea	1.57e+03
	41	12	44.4	28	9	Q49288	ced-4 primer.	1.57e+03
	42	12	44.4	41	51	V51151	Maize polymorphic mar	1.57e+03
c	43	12	44.4	43	44	V27600	F1.2 C9 region oligon	1.57e+03

Note: Post-processor removed 955 summaries from list due to search parameters cho...

ALIGNMENTS

RESULT 1
ID V66349 standard; DNA; 50 BP.
AC V66349;
DT 06-JAN-1999 (first entry)
DE CML-2 chromosomal translocation t(9;22) primer.
KW CML-2 chromosomal translocation t(9; 22); block splice template;
KW autocatalytic RNA amplification; primer; ss.
OS Synthetic.
PN US5824518-A.
PD 20-OCT-1998.
PF 06-JUN-1995; 469067.
PR 10-JUL-1990; US-550837.
PR 11-JUL-1989; US-379501.
PR 06-JUN-1995; US-469067.
PA (GENP-) GEN-PROBE INC.
PI Fultz TJ, Kacian DL;
DR WPI; 98-582557/49.
PT Block splice template useful for amplification of nucleic acids -
PT comprises two nucleic acid regions, the first region located 3' of
PT the second region and blocked at its 3' terminus to inhibit primer
PT extension by a DNA polymerase
PS Example 15; Column 9; 51pp; English.
CC V66349-50 represent CML-2 chromosomal translocation t(9;22) primers,
CC for the (+) and (-) strands respectively. The primers are used to
CC exemplify the invention, together with probe V66351. The specification
CC describes methods of synthesising multiple copies of a target nucleic
CC acid sequence autocatalytically under conditions of substantially
CC constant temperature, ionic strength and pH are provided in which
CC multiple RNA copies of the target sequence autocatalytically
CC generate additional copies. The target sequence is a block splice
CC template which comprises two nucleic acid regions. The first region is
CC located 3' of the second region and is blocked at its 3' terminus to

```
CC   inhibit primer extension by a DNA polymerase, and the second region
CC   comprises a promoter sequence recognised by an RNA polymerase. The
CC   methods are used to amplify nucleic acids, especially RNA, for
CC   analysis, cloning or probe production.
SQ   Sequence   50 BP;    17 A;    12 C;    11 G;    10 T;

  Query Match           88.9%;  Score 24;  DB 51;  Length 50;
  Best Local Similarity 100.0%;  Pred. No. 1.07e-03;
  Matches   24;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db     27 actcagaccctgaggctcaaagtc 50
          ||||||||||||||||||||||||
Cp     27 ACTCAGACCCTGAGGCTCAAAGTC 4


RESULT    2
ID   T15571 standard; DNA; 50 BP.
AC   T15571;
DT   17-JUL-1996  (first entry)
DE   CML-2 chromosomal translocation major breakpoint t(9;22) (-) primer.
KW   CML-2 chromosomal translocation major breakpoint; t(9;22); primer;
KW   auto-catalytic; synthesis; RNA target sequence; assay; detection;
KW   quantification; ss.
OS   Synthetic.
PN   US5480784-A.
PD   02-JAN-1996.
PF   11-JUL-1989; 379501.
PR   11-JUL-1989; US-379501.
PR   10-JUL-1990; US-550837.
PA   (GENP-) GEN-PROBE INC.
PI   Fultz TJ,  Kacian DL;
DR   WPI; 96-068248/07.
PT   Auto-catalytic synthesis of multiple copies of an RNA target
PT   sequence - uses cooperative action of a DNA and RNA polymerase in
PT   presence of RNase H, useful for detection of target sequence e.g. in
PT   clinical or environmental sample
PS   Example; Columns 9-10; 51pp; English.
CC   The present sequence is a primer for the CML-2 chromosomal
CC   translocation major breakpoint t(9;22), which was used to
CC   demonstrate an improved method for synthesising multiple copies of
CC   a RNA target sequence. The method comprises combining the target
CC   with a primer which hybridises to the 3'-terminal portion of the
CC   target, a promoter primer which hybridises with a portion of the
CC   DNA primer extension prod., reverse transcriptase, RNase H and
CC   transcriptase. It can be used as a component of an assay to detect
CC   and/or quantitate specific target sequences in clinical,
CC   environmental or forensic samples. It also has the advantages of
CC   being autocatalytic, using the cooperative action of a DNA
CC   polymerase, e.g. a reverse transcriptase and avoids repetitive
CC   manipulations of reaction conditions, e.g. temp., ionic strength
CC   and pH.
SQ   Sequence   50 BP;    17 A;    12 C;    11 G;    10 T;

  Query Match           88.9%;  Score 24;  DB 19;  Length 50;
  Best Local Similarity 100.0%;  Pred. No. 1.07e-03;
  Matches   24;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db     27 actcagaccctgaggctcaaagtc 50
          ||||||||||||||||||||||||
Cp     27 ACTCAGACCCTGAGGCTCAAAGTC 4


RESULT    3
ID   T42417 standard; DNA; 50 BP.
AC   T42417;
DT   28-APR-1997  (first entry)
DE   CML chromosomal translocation primer #1.
KW   HIV; probe; primer; amplify; polymerase chain reaction; microorganism;
KW   BCL-2; PCR; hepatitis B virus; HBV; CML; ss.
OS   Synthetic.
PN   EP-731175-A2.
PD   11-SEP-1996.
PF   10-JUL-1990; 307503.
PR   11-JUL-1989; US-379501.
PA   (GENP-) GEN-PROBE INC.
PI   Mcdonough S;
DR   WPI; 96-403995/41.
PT   Detection of HIV nucleic acids in samples - using new specific
PT   oligo-nucleotide(s) for the amplification and detection of target
PT   sequences.
PS   Disclosure; Page 8; 66pp; English.
CC   T42417-T42419 represent primers and a probe for the CML chromosomal
CC   translocation t(9;22).  These sequences can be used in modified versions
CC   of the kits of the invention.  The kits of the invention, are for
CC   detecting the presence of HIV nucleic acid sequences in a sample.  The
CC   kits comprise two amplification primers (such as T40182 and T40183),
CC   a probe (such as T42404) for detection of the amplified sequence.  The
CC   using these sequences, the amplification of HIV nucleic acid from
CC   improved.  The kits can also be used for the detection of other
CC   microorganisms, by using different probe sequences.  Other sequences
CC   can be detected using this method include those from HBV (using the
CC   sequences shown in T42410-T42412), and BCL-2 (using T42413-T42416).  The
CC   samples can be clinical, environmental or forensic samples, and the
CC   method produces large amounts of the target sequence for a variety of
CC   uses.  The method can also be used to produce multiple copies of a target
CC   sequence for use in cloning, and sequencing, and to produce probes for
CC   the target sequence.
SQ   Sequence   50 BP;    17 A;    12 C;    11 G;    10 T;

  Query Match           88.9%;  Score 24;  DB 28;  Length 50;
  Best Local Similarity 100.0%;  Pred. No. 1.07e-03;
  Matches   24;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db     27 actcagaccctgaggctcaaagtc 50
          ||||||||||||||||||||||||
Cp     27 ACTCAGACCCTGAGGCTCAAAGTC 4


RESULT    4
ID   Q86626 standard; DNA; 50 BP.
AC   Q86626;
DT   15-NOV-1995  (first entry)
DE   CML chromosomal translocation minus strand primer.
KW   Primer; autocatalytic; target; CML; translocation; ss.
OS   Synthetic.
PN   US5399491-A.
PD   21-MAR-1995.
PF   11-JUL-1989; 379501.
PR   11-JUL-1989; US-379501.
PR   10-JUL-1990; US-550837.
PR   19-MAR-1992; US-855732.
PA   (GENP-) GEN-PROBE INC.
PI   Fultz TJ,  Kacian DL;
DR   WPI; 95-130686/17.
PT   Amplification of nucleic acid targets - using a reverse
PT   transcriptase with RNase H activity and a RNA polymerase at
PT   constant temp.
PS   Disclosure; Column 9; 58pp; English.
CC   Q86626-28 are primers and a probe for the CML chromosomal
CC   translocation. They are used to produce autocatalytic
CC   oligonucleotides which require no change in the experimental
CC   conditions i.e.constant temperature, pH and ionic strength.
CC   These sequences are useful in generating multiple copies of
CC   specific nucleic acid target sequences.
SQ   Sequence   50 BP;    17 A;    12 C;    11 G;    10 T;

  Query Match           88.9%;  Score 24;  DB 15;  Length 50;
  Best Local Similarity 100.0%;  Pred. No. 1.07e-03;
  Matches   24;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps

Db     27 actcagaccctgaggctcaaagtc 50
          ||||||||||||||||||||||||
Cp     27 ACTCAGACCCTGAGGCTCAAAGTC 4


RESULT    5
```

```
ID   Q14244 standard; DNA; 22 BP.
AC   Q14244;
DT   20-JAN-1992  (first entry)
DE   Primer CMLII.
KW   Acute lymphocytic leukaemia; chimeric; mRNA; ABL; breakpoint;
KW   cluster; BCR; ALL; exon junction; PCR; ss.
OS   Synthetic.
PN   US5057410-A.
PD   15-OCT-1991.
PF   05-AUG-1988; 229604.
PR   05-AUG-1988; US-229604.
PA   (CETU ) CETUS CORP.
PI   Kawasaki ES, McCormick EP, Witto OO;
DR   WPI; 91-324515/44.
PT   Method for detecting chimeric mRNA - useful e.g. for
PT   distinguishing between acute lymphocytic leukaemia and chronic
PT   myeloid leukaemia.
PS   Claim 5; Page 13; 14pp; English.
CC   The primer is used with primer CMLI (Q14243) to amplify chimeric
CC   mRNA contg. a specific exon-exon junction associated with chronic
CC   myeloid leukaemia (CML).  It is complementary to cDNA sequences
CC   within the ABL exon II.  It can distinguish between ALL BCR-ABL
CC   chimeric mRNA and CML BCR-ABL mRNA.  The CML DNA sequences used
CC   to design the primer are reported by Heisterkamp, N., et al.
CC   Nature 315 :758 (1985); Grosvelt, G., at al Mol. Cell Biol. 6:607
CC   (1987); and Shtivelman, E., et al Cell 47:277 (1986).
CC   See also Q14241-47.
SQ   Sequence   22 BP;    6 A;    7 C;    5 G;    4 T;

  Query Match           81.5%;  Score 22;  DB 3;  Length 22;
  Best Local Similarity 100.0%;  Pred. No. 1.41e-02;
  Matches   22;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db       1 tcagaccctgaggctcaaagtc 22
           ||||||||||||||||||||||
Cp      25 TCAGACCCTGAGGCTCAAAGTC 4

RESULT    6
ID   Q62302 standard; DNA; 22 BP.
AC   Q62302;
DT   02-NOV-1994  (first entry)
DE   PCR primer for amplifying bcr/abl oncogene.
KW   oncogene; amplification; polymerase chain reaction; PCR; blood;
KW   reverse transcription; primer; ss.
OS   Synthetic.
PN   US5300635-A.
PD   05-APR-1994.
PF   01-FEB-1993; 013419.
PR   01-FEB-1993; US-013419.
PA   (IOWA ) UNIV IOWA STATE RES FOUND INC.
PI   Macfarlane DE;
DR   WPI; 94-125850/15.
PT   Use of quaternary amine surfactants - for isolating nucleic acids
PT   from a biological sample by forming complexes which can be
PT   dissociated
PS   Example 11; Column 11; 8pp; English.
CC   Two primers (Q62302, Q62303) were used to amplify the bcr/abl
CC   oncogene.  The amplification was performed to demonstrate that
CC   isolation of RNA from whole blood by the cationic surfactant method
CC   produces RNA which can be reverse transcribed and amplified without
CC   the need for further purification.
SQ   Sequence   22 BP;    6 A;    7 C;    5 G;    4 T;

  Query Match           81.5%;  Score 22;  DB 10;  Length 22;
  Best Local Similarity 100.0%;  Pred. No. 1.41e-02;
  Matches   22;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db       1 tcagaccctgaggctcaaagtc 22
           ||||||||||||||||||||||
Cp      25 TCAGACCCTGAGGCTCAAAGTC 4

RESULT    7
ID   T88787 standard; DNA; 22 BP.
AC   T88787;
DT   23-MAR-1998  (first entry)
DE   Leukaemic cell BCR-ABL target sequence detection probe.
KW   Leukaemia; BCR-ABL; cell line K562; target; immunoassay; probe;
KW   hybridisation; diagnostic; luciferase; genetic disease; ss.
OS   Synthetic.
PN   CA2186998-A.
PD   31-MAY-1997.
PF   02-OCT-1996; 186998.
PR   30-NOV-1995; US-565055.
PA   (UYWI-) UNIV WINDSOR.
PI   Christopoulos TK;
DR   WPI; 97-415964/39.
PT   Immunoassays and nucleic acid hybridisation assays - using
PT   protein-encoding nucleic acid fragments as labels
PS   Disclosure; Page 26; 39pp; English.
CC   A novel assay has been developed for determining an analyte. The assay
CC   comprises labelling the analyte with a nucleic acid fragment that
CC   encodes a protein, expressing the nucleic acid, and detecting the
CC   protein. The present sequence represents a detection probe for a BCR-ABL
CC   target sequence from a leukaemic cell (cell line K562), used in an
CC   example of the present assay. The assay is used for the determination
CC   of antigens or nucleic acids for diagnostic or research purposes, e.g.
CC   detecting low levels of tumour markers, analysing nucleic acid mutations
CC   associated with genetic diseases, diagnosing and monitoring pathogen
CC   infections, or searching for new disease markers. The immunoassay when
CC   using a luciferase for detection is more sensitive than an enzyme-
CC   amplified, time-resolved fluorometric immunoassay and does not require
CC   preparation of a luciferase-antibody conjugate.
SQ   Sequence   22 BP;    6 A;    7 C;    5 G;    4 T;

  Query Match           81.5%;  Score 22;  DB 36;  Length 22;
  Best Local Similarity 100.0%;  Pred. No. 1.41e-02;
  Matches   22;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db       1 tcagaccctgaggctcaaagtc 22
           ||||||||||||||||||||||
Cp      25 TCAGACCCTGAGGCTCAAAGTC 4

RESULT    8
ID   V01841 standard; DNA; 50 BP.
AC   V01841;
DT   04-JUN-1998  (first entry)
DE   PCR primer abl50 used to produce antisense RNA and ribozyme sequences.
KW   Antisense; inhibitor; gene expression; chromosomal translocation;
KW   translocation point; pharmaceutical composition; bcr; bcr-abl;
KW   chronic myelogenous leukaemia; acute lymphoblastic leukaemia;
KW   acute myelogenous leukaemia; Non-Hodgkin lymphoma; treatment;
KW   PCR primer; amplify; ss.
OS   Synthetic.
PN   WO9746672-A2.
PD   11-DEC-1997.
PF   05-JUN-1997; EC0323.
PR   05-JUN-1996; EP-009034.
PA   (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PI   Haas R, Kronenwett R, Sczakiel G;
DR   WPI; 98-042181/04.
PT   Nucleic acid molecule containing chromosomal translocation point -
PT   useful to treat chromosomal translocation disorders, e.g. chronic
PT   myelogenous leukaemia
PS   Disclosure; Page 22; 49pp; English.
CC   PCR primers V01837-43 were used to amplify bcr and bcr-abl sequences from
CC   reverse transcribed mRNA isolated from the human Philadelphia-positive
CC   (Ph+) cell line K562. The PCR products were used as a template for in
CC   vitro synthesis of antisense RNA and ribozymes. Antisense molecules and
CC   ribozymes are potent inhibitors of gene expression and viral functions.
CC   The antisense molecules V01779-804 and the ribozymes V01805-32 exemplify
CC   novel nucleic acid molecules of the invention. These nucleic acid
CC   molecules contain portions complementary to a first and second
CC   chromosomal DNA sequence. The nucleic acid molecule forms at least part
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CC   of a chromosomal translocation resulting in a fusion gene containing the
CC   translocation point. The DNA sequence, as well as vectors and host cells
CC   containing it are useful in pharmaceutical compositions for treating
CC   disorders based on chromosomal translocations, preferably for chronic
CC   myelogenous leukaemia. The pharmaceutical composition may also be used
CC   to treat acute lymphoblastic leukaemias, acute myelogenous leukaemias
CC   and Non-Hodgkin lymphomas.
SQ   Sequence   50 BP;    15 A;    14 C;    11 G;    10 T;

  Query Match          74.1%;  Score 20;  DB 40;  Length 50;
  Best Local Similarity 100.0%;  Pred. No. 1.73e-01;
  Matches   20;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db      31 actcagaccctgaggctcaa 50
           ||||||||||||||||||||
Cp      27 ACTCAGACCCTGAGGCTCAA 8


RESULT    9
ID   V58784 standard; DNA; 24 BP.
AC   V58784;
DT   10-DEC-1998  (first entry)
DE   Detection probe for BCR/ABL type chimera mRNA.
KW   Probe; BCR/ABL type chimera; chimera detection; Major-bcr;
KW   nucleic acid strand based amplification; NASBA method; ss.
OS   Synthetic.
PN   J10229899-A.
PD   02-SEP-1998.
PF   21-FEB-1997; 054092.
PR   21-FEB-1997; JP-054092.
PA   (SRLS-) SRL KK.
PA   (TOYM ) TOYOBO KK.
DR   WPI; 98-524294/45.
PT   Forward side primer and reverse side primer - used for detection of
PT   BCR/ABL type chimera mRNA easily with high sensitivity
PS   Example 1; Page 6; 8pp; Japanese.
CC   This sequence represents a probe for Major-bcr mRNA. The invention
CC   relates to a method for the detection of a BCR/ABL type chimera mRNA with
CC   a cleavage point in Major-bcr by using primers in a
CC   nucleic acid strand based amplification (NASBA) method. The primers can
CC   be used to detect BCR/ABL type chimera mRNA easily with high sensitivity.
SQ   Sequence   24 BP;    5 A;    6 C;    6 G;    7 T;

  Query Match          70.4%;  Score 19;  DB 50;  Length 24;
  Best Local Similarity 68.4%;  Pred. No. 5.93e-01;
  Matches   13;  Conservative    6;  Mismatches   0;  Indels   0;  Gaps   0;

Db       6 tctgactttgagcctcagg 24
           :|:|||:::|||||:||||
Qy       1 UCUGACUUUGAGCCUCAGG 19


RESULT   10
ID   Q86124 standard; RNA; 23 BP.
AC   Q86124;
DT   16-NOV-1995  (first entry)
DE   bcr-abl mRNA junction fragment primer #2.
KW   Catalytically active fragment; synthetic ribozyme subunit; neoplasm;
KW   hybrid oncogene; chromosomal translocation; oncogene mRNA transcript;
KW   flanking sequence; leukaemia; bone marrow cell; PCR; primer; ss.
OS   Synthetic.
PN   WO9507923-A.
PD   23-MAR-1995.
PF   31-AUG-1994; U09963.
PR   15-SEP-1993; US-122795.
PA   (UTEM ) UNIV TEMPLE.
PI   Leopold LH,  Reddy EP,  Reddy MVR,  Shore SK;
DR   WPI; 95-131308/17.
PT   New multi:unit ribozyme which cleaves hybrid oncogene transcripts
PT   - for treating neoplasms characterised by chromosomal
PT   trans:location(s), esp. leukaemia
PS   Example 7; Page 26; 44pp; English.
CC   The sequences given in Q86123-25 represent primers and a probe which
CC   were used in the isolation of the bcr-abl mRNA. The isolated mRNA
CC   was used to test the synthetic RNA molecule of the invention which is
CC   useful for the treatment of neoplasm. The neoplasm to be treated is
CC   characterised by the presence of a hybrid oncogene caused by
CC   chromosomal translocation. The synthetic RNA molecule comprises at
CC   least three ribozyme subunits each of which comprises a first
CC   flanking sequence which has a nucleotide sequence complementary to,
CC   and hybridisable with, the nucleotide sequence of a portion of the
CC   oncogene mRNA transcript substantially 5' of the oncogene translocation
CC   junction and a second flanking sequence which has a nucleotide sequence
CC   complementary to, and hybridisable with, the nucleotide sequence of a
CC   portion of the oncogene mRNA transcript substantially 3' of the oncogene
CC   translocation junction and a catalytically active segment disposed
CC   between the first and second flanking segments comprising a ribozyme
CC   capable of cleaving the oncogene on or near the translocation junction.
CC   The synthetic RNA's can br used to treat neoplasms, esp. leukaemia.  The
CC   patients cells may be treated in vivo or cells, esp. bone marrow cells,
CC   are aspirated, treated and returned to the patient.
SQ   Sequence   23 BP;    6 A;    7 C;    5 G;    5 T;

  Query Match          63.0%;  Score 17;  DB 15;  Length 23;
  Best Local Similarity 94.7%;  Pred. No. 6.51e+00;
  Matches   18;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db       1 tcagaccctgaggctctaa 19
           |||||||||||||||| ||
Cp      25 TCAGACCCTGAGGCTCAAA 7


RESULT   11
ID   T62502 standard; DNA; 27 BP.
AC   T62502;
DT   28-APR-1997  (first entry)
DE   Murine retrovirus consensus right side integration response sequence.
KW   Consensus sequence; right side; integration response; LTR;
KW   long terminal repeat; retroviral attachment sequence; preparation;
KW   gene delivery construct; ss.
OS   Murine retrovirus.
PN   WO9626745-A1.
PD   06-SEP-1996.
PF   28-FEB-1996; U02877.
PR   28-FEB-1995; US-395355.
PA   (UYCR-) UNIV CREIGHTON.
PI   Hodgson CP;
DR   WPI; 96-412589/41.
PT   Gene delivery system including liposome or dendrimer and
PT   perpetuation molecule  - esp. for gene therapy, provides efficient
PT   and stable expression of chimeric genes more safely than use of
PT   viruses.
PS   Example 3; Fig 2; 50pp; English.
CC   The present sequence is the murine retrovirus consensus right side
CC   (U5) integration response sequence, which reads towards the outside
CC   of the long terminal repeat (LTR). It can be used as a retroviral
CC   attachment sequence in the preparation of a gene delivery construct
SQ   Sequence   27 BP;    1 A;    2 C;    0 G;    6 T;

  Query Match          63.0%;  Score 17;  DB 28;  Length 27;
  Best Local Similarity 10.0%;  Pred. No. 6.51e+00;
  Matches    2;  Conservative   16;  Mismatches   2;  Indels   0;  Gaps   0;

Db       1 drvbnsbshhhhyyvrrrtc 20
           :::: :::: ::::::::||
Cp      23 AGACCCTGAGGCTCAAAGTC 4


RESULT   12
ID   T62502 standard; DNA; 27 BP.
AC   T62502;
DT   28-APR-1997  (first entry)
DE   Murine retrovirus consensus right side integration response sequence.
KW   Consensus sequence; right side; integration response; LTR;
KW   long terminal repeat; retroviral attachment sequence; preparation;
KW   gene delivery construct; ss.
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OS   Murine retrovirus.
PN   WO9626745-A1.
PD   06-SEP-1996.
PF   28-FEB-1996; U02877.
PR   28-FEB-1995; US-395355.
PA   (UYCR-) UNIV CREIGHTON.
PI   Hodgson CP;
DR   WPI; 96-412589/41.
PT   Gene delivery system including liposome or dendrimer and
PT   perpetuation molecule - esp. for gene therapy, provides efficient
PT   and stable expression of chimeric genes more safely than use of
PT   viruses.
PS   Example 3; Fig 2; 50pp; English.
CC   The present sequence is the murine retrovirus consensus right side
CC   (U5) integration response sequence, which reads towards the outside
CC   of the long terminal repeat (LTR). It can be used as a retroviral
CC   attachment sequence in the preparation of a gene delivery construct.
SQ   Sequence   27 BP;    1 A;    2 C;    0 G;    6 T;

  Query Match           59.3%;  Score 16;  DB 28;  Length 27;
  Best Local Similarity  4.8%;  Pred. No. 2.08e+01;
  Matches     1;  Conservative   17;  Mismatches   3;  Indels   0;  Gaps   0;

Db       1 drvbnsbshhbhyyvrrrtct 21
           ::::  ::: ::::::::::|: 
Qy       3 UGACUUUGAGCCUCAGGGUCU 23


RESULT   13
ID   T91968 standard; RNA; 16 BP.
AC   T91968;
DT   13-FEB-1998  (first entry)
DE   RNA sequence disclosed in patent on miniribozymes.
KW   miniribozyme; ribozyme; dimer; cleavage; disease; treatment; ss.
OS   Synthetic.
PN   J09224673-A.
PD   02-SEP-1997.
PF   22-FEB-1996; 034898.
PR   22-FEB-1996; JP-034898.
PA   (AGEN ) AGENCY OF IND SCI & TECHNOLOGY.
PA   (HITB ) HITACHI CHEM CO LTD.
PA   (TAIS ) TAISHO PHARM CO LTD.
DR   WPI; 97-553198/51.
PT   Two mini ribozymes which hybridise to form a new heterodimer -
PT   useful for cleavage and inactivation of a target DNA, especially for
PT   diagnosis and treatment of genetic disease
PS   Disclosure; Page 12; 15pp; Japanese.
CC   The following mini-ribozymes of formulae (I) and (II) are new:
CC   3'-Q1n...Q12 Q11 A A A G L V Q21 Q22...Q2m-5' (I); and
CC   3'-R1n...R12 R11 W M A G Y A G U C  R21 R22...R2m-5' (II).
CC   Y = A, G, C or U; L = (3')-C-(5') and M = (3')-G-(5') or
CC   L = (3')-C Np-(5') and M = (3')-N'p G-(5'); N = A, U, G or C and
CC   N' = the complementary nucleotides of N; p = 1-10 (same for both N and
CC   N'); V = (3')-AGYAGUC-(5') and W = (3')-AAG-(5') or V,W = a bond;
CC   Q and R are RNA or DNA mononucleotides complementary to a target RNA;
CC   Q1n,...Q12 Q11 with R1n...R12 R11 and Q21 Q22...Q2m with R21 R22...R2m
CC   are same or different; m, n = an integer.  Miniribozyme dimers of the
CC   formula (I/II) are also claimed and have a two-part binding region for
CC   target RNA and L and M are base-paired to form a stem structure. The
CC   mini-ribozymes and the dimer they form can be used for cleavage and
CC   inactivation of RNA. They are also useful as agents for treatment or
CC   diagnosis of a genetic disease. The present sequence was disclosed
CC   in the sequence ID listing of the specification.
SQ   Sequence   16 BP;    2 A;    4 C;    6 G;    4 U;

  Query Match           55.6%;  Score 15;  DB 35;  Length 16;
  Best Local Similarity 100.0%;  Pred. No. 6.46e+01;
  Matches    15;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db       1 ccucagggucugagu 15
           ||||||||||||||| 
Qy      13 CCUCAGGGUCUGAGU 27


RESULT   14
ID   Q51057 standard; DNA; 20 BP.
AC   Q51057;
DT   11-MAY-1994  (first entry)
DE   Human glucokinase exon 1a PCR-SSCP analysis downstream primer.
KW   Human; glucokinase; short arm; chromosome 7; MODY; insulin secretion;
KW   non-insulin dependant diabetes mellitus; NIDDM; glucose-6-phosphate;
KW   maturity-onset diabetes of the young; glucose; regulation; mutation;
KW   detection; primer; amplify; single-strand conformational polymorphism;
KW   adenosine deaminase; ADA; GLUT2; beta-cell glucose transporter;
KW   restriction fragment length polymorphism; polymerase chain reaction;
KW   RFLP; SSCP; exon; PCR; ss.
OS   Synthetic.
PN   WO9321343-A.
PD   28-OCT-1993.
PF   14-APR-1993; U03560.
PR   22-APR-1992; US-872678.
PA   (ARCH-) ARCH DEV CORP.
PI   Bell GI,  Cohen D,  Froguel P,  Pilleis SJ,  Stoffel M;
PI   Takeda J, Velho G,  Vionnet N,  Yasuda K,  Zouali H;
DR   WPI; 93-351752/44.
PT   Detection of early onset, non-insulin dependent diabetes mellitus
PT   - by detecting a mutation in a glucokinase gene or prod., esp.
PT   for maturity onset diabetes of the young
PS   Example 7; Page 81; 60pp; English.
CC   The sequences given in Q51045-79 are primers which were used in the
CC   detection of restriction fragment length polymorphisms (RFLPs) within
CC   the human adenosine deaminase gene (ADA), beta-cell glucose transporter
CC   gene (GLUT2) and the human glucokinase gene.  The glucokinase gene maps
CC   to a locus on the short arm of chromosome 7 and mutations within this
CC   gene show some correlation with certain forms of non-insulin dependant
CC   diabetes mellitus (NIDDM), esp. maturity-onset diabetes of the young
CC   (MODY).  The polymorphic AluVpA region of ADA cosegregates with one
CC   gene responsible for MODY and has been mapped to the long arm of
CC   chromosome 20.  Glucokinase is an enzyme which catalyses the formation
CC   of glucose-6-phosphate from glucose and may be involved in the
CC   regulation of insulin secretion and integration of hepatic intermediary
CC   metabolism.  Nonsense and missense mutations within the glucokinase
CC   gene (see also Q51038-44) may be identified by the method of the
CC   invention.  Early onset NIDDM is examined by detecting at least one
CC   single nucleotide change in a portion of the gene. The DNA is isolated
CC   and a pair of primers are selected which are capable of amplifying an
CC   exon of the gene via PCR.  The single nucleotide changes are identified
CC   in the amplification product.
SQ   Sequence   20 BP;    6 A;    5 C;    4 G;    5 T;

  Query Match           55.6%;  Score 15;  DB 9;  Length 20;
  Best Local Similarity 89.5%;  Pred. No. 6.46e+01;
  Matches    17;  Conservative    0;  Mismatches   2;  Indels   0;  Gaps   0;

Db       1 tcagattctcaggctcaaa 19
           |||||  ||||||||||||| 
Cp      25 TCAGACCCTGAGGCTCAAA 7


RESULT   15
ID   V39479 standard; DNA; 20 BP.
AC   V39479;
DT   22-SEP-1998  (first entry)
DE   Chronic myelogenous/acute lymphocytic leukaemia detection probe.
KW   Acute lymphocytic leukaemia; Chronic myelogenous leukaemia; ALL; CML;
KW   target; capture probe; detection probe; hybridisation; bcr; abl;
KW   multiple analyte; Salmonella; chromasomal translocation;
KW   Philadelphia chromosome; ss.
OS   Synthetic.
OS   Homo sapiens.
PN   EP-846776-A2.
PD   10-JUN-1998.
PF   05-DEC-1997; 309831.
PR   06-DEC-1996; US-761131.
PA   (VYSI-) VYSIS INC.
PI   Lane DJ, Muller CR;
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DR   WPI; 98-299988/27.
PT   Assay device for isolating analyte from sample, e.g. Salmonella in
PT   food - comprises tube containing linear array of binding elements,
PT   linked to binding factor to which component binds
PS   Example 2; Page 13; 25pp; English.
CC   An assay device has been developed for isolating an analyte from a
CC   sample. The assay device comprises a tube containing a linear array of
CC   binding elements, each linked to a distinct binding factor to which a
CC   corresponding specific component binds, where each of the binding
CC   elements is configured to sealingly contact the interior surface of the
CC   tube along the entire circumference of the binding element. The present
CC   sequence represents a detection probe used in an example from the present
CC   invention for the detection of chromosomal translocations. The new
CC   method and device can be used to detect e.g. Salmonella in a food
CC   sample. They are also used to detect chromasomal translocations to
CC   detect the 'Philadelphia' chromosome responsible for acute lymphocytic
CC   leukaemia and chronic myelogenous leukaemia.
SQ   Sequence   20 BP;    7 A;    4 C;    5 G;    4 T;

  Query Match           55.6%;  Score 15;  DB 45;  Length 20;
  Best Local Similarity 100.0%;  Pred. No. 6.46e+01;
  Matches   15;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db      1 aggctcaaagtcaga 15
          ||||||||||||||||
Cp     15 AGGCTCAAAGTCAGA 1


RESULT   16
ID   V39474 standard; DNA; 40 BP.
AC   V39474;
DT   22-SEP-1998  (first entry)
DE   Chronic myelogenous leukaemia model target oligonucleotide.
KW   Acute lymphocytic leukaemia; Chronic myelogenous leukaemia; ALL; CML;
KW   target; capture probe; detection probe; hybridisation; bcr; abl;
KW   multiple analyte; Salmonella; chromasomal translocation;
KW   Philadelphia chromosome; ss.
OS   Synthetic.
OS   Homo sapiens.
PN   EP-846776-A2.
PD   10-JUN-1998.
PF   05-DEC-1997; 309831.
PR   06-DEC-1996; US-761131.
PA   (VYSI-) VYSIS INC.
PI   Lane DJ, Muller UR;
DR   WPI; 98-299988/27.
PT   Assay device for isolating analyte from sample, e.g. Salmonella in
PT   food - comprises tube containing linear array of binding elements,
PT   linked to binding factor to which component binds
PS   Example 2; Page 12; 25pp; English.
CC   An assay device has been developed for isolating an analyte from a
CC   sample. The assay device comprises a tube containing a linear array of
CC   binding elements, each linked to a distinct binding factor to which a
CC   corresponding specific component binds, where each of the binding
CC   elements is configured to sealingly contact the interior surface of the
CC   tube along the entire circumference of the binding element. The present
CC   sequence represents a model target used in an example from the present
CC   invention for the detection of chromosomal translocations. The new
CC   method and device can be used to detect e.g. Salmonella in a food
CC   sample. They are also used to detect chromasomal translocations to
CC   detect the 'Philadelphia' chromosome responsible for acute lymphocytic
CC   leukaemia and chronic myelogenous leukaemia.
SQ   Sequence   40 BP;    10 A;    10 C;    8 G;    12 T;

  Query Match           55.6%;  Score 15;  DB 45;  Length 40;
  Best Local Similarity 60.0%;  Pred. No. 6.46e+01;
  Matches    9;  Conservative    6;  Mismatches   0;  Indels   0;  Gaps   0;

Db     26 tctgactttgagcct 40
          :|:|||:::|||||:
Qy      1 UCUGACUUUGAGCCU 15


RESULT   17
ID   V39473 standard; DNA; 40 BP.
AC   V39473;
DT   22-SEP-1998  (first entry)
DE   Acute lymphocytic leukaemia model target oligonucleotide.
KW   Acute lymphocytic leukaemia; Chronic myelogenous leukaemia; ALL; CML;
KW   target; capture probe; detection probe; hybridisation; bcr; abl;
KW   multiple analyte; Salmonella; chromasomal translocation;
KW   Philadelphia chromosome; ss.
OS   Synthetic.
OS   Homo sapiens.
PN   EP-846776-A2.
PD   10-JUN-1998.
PF   05-DEC-1997; 309831.
PR   06-DEC-1996; US-761131.
PA   (VYSI-) VYSIS INC.
PI   Lane DJ, Muller UR;
DR   WPI; 98-299988/27.
PT   Assay device for isolating analyte from sample, e.g. Salmonella in
PT   food - comprises tube containing linear array of binding elements,
PT   linked to binding factor to which component binds
PS   Example 2; Page 12; 25pp; English.
CC   An assay device has been developed for isolating an analyte from a
CC   sample. The assay device comprises a tube containing a linear array of
CC   binding elements, each linked to a distinct binding factor to which a
CC   corresponding specific component binds, where each of the binding
CC   elements is configured to sealingly contact the interior surface of the
CC   tube along the entire circumference of the binding element. The present
CC   sequence represents a model target used in an example from the present
CC   invention for the detection of chromosomal translocations. The new
CC   method and device can be used to detect e.g. Salmonella in a food
CC   sample. They are also used to detect chromasomal translocations to
CC   detect the 'Philadelphia' chromosome responsible for acute lymphocytic
CC   leukaemia and chronic myelogenous leukaemia.
SQ   Sequence   40 BP;    10 A;    13 C;    7 G;    10 T;

  Query Match           55.6%;  Score 15;  DB 45;  Length 40;
  Best Local Similarity 60.0%;  Pred. No. 6.46e+01;
  Matches    9;  Conservative    6;  Mismatches   0;  Indels   0;  Gaps   0;

Db     26 tctgactttgagcct 40
          :|:|||:::|||||:
Qy      1 UCUGACUUUGAGCCU 15


RESULT   18
ID   Q56492 standard; DNA; 48 BP.
AC   Q56492;
DT   25-JUL-1994  (first entry)
DE   PCR primer for K552 cell line used in 3SR amplification reaction.
KW   PCR; polymerase chain reaction; amplification; detection;
KW   translocation; point mutation; RNA; ribonucleic acid; in situ; ss.
OS   Synthetic.
PN   WO9402644-A.
PD   03-FEB-1994.
PF   16-JUL-1993; U00716.
PR   17-JUL-1992; US-915894.
PR   17-JUL-1992; US-915893.
PR   17-JUL-1992; US-915900.
PR   17-JUL-1992; US-916183.
PR   17-JUL-1992; US-915927.
PR   17-JUL-1992; US-916068.
PA   (APRO-) APROGENEX INC.
PA   (BAXT ) BAXTER DIAGNOSTICS INC.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Asgari M,  Blick M,  Bresser J,  Colvin D,  Cubbage ML;
PI   Haydock PV, Ju SC,  Jurtshuk R,  Prashad N,  Reading CL;
PI   Weber WD;
DR   WPI; 94-048901/06.
PT   Detection of RNA in cells or viruses - by means of in-situ 3SR
PT   amplification
PS   Example 1; Page 78; 88pp; English.
CC   The 3SR amplification procedure allows the detection of a target RNA
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CC   molecule in a biological entity i.e RNA detection within cells or
CC   viruses. The process is especially useful for detecting RNA
CC   molecules that only occur in cells that have undergone chromosomal
CC   translocation (especially tumour cells) and RNA molecules
CC   transcribed from point mutated DNA segments. Two primers (Q56491,
CC   Q56492) were used to amplify RNA from the K562 human chronic
CC   myelogenous leukaemia-blast crisis cell line for the subsequent
CC   detection of a translocation.
SQ   Sequence   48 BP;    14 A;    12 C;    10 G;    12 T;

  Query Match           55.6%;  Score 15;  DB 10;  Length 48;
  Best Local Similarity 100.0%;  Pred. No. 6.46e+01;
  Matches    15;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db      34 actcagaccctgagg 48
           |||||||||||||||
Cp      27 ACTCAGACCCTGAGG 13


RESULT   19
ID   T38971 standard; DNA; 29 BP.
AC   T38971;
DT   29-MAY-1997  (first entry)
DE   Interleukin IL-3 3' PCR primer.
KW   Cytokine; expression profile; genital wart; interleukin 12; IL-12;
KW   tumour regression; adjuvant; polymerase chain reaction; PCR;
KW   condyloma acuminata; human papilloma virus; HPV-6; HPV-11; HPV16;
KW   HPV18; anogenital; cutaneous; laryngeal; oesophageal; cancer; ss.
OS   Synthetic.
PN   WO9629091-A1.
PD   26-SEP-1996.
PF   22-MAR-1996; G00686.
PR   22-MAR-1995; GB-005784.
PA   (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
PI   Scarpini CG,  Stanley MA;
DR   WPI; 96-442947/44.
PT   Use of interleukin-12 to treat papilloma virus-associated lesions -
PT   esp. as a vaccine adjuvant with papilloma virus antigen for
PT   immuno:therapy of warts or tumours
PS   Disclosure; Page 14; 32pp; English.
CC   RNA was extracted from genital lesions, reverse transcribed to
CC   produce cDNA and then the cDNA was used as the template for PCR
CC   amplification of various cytokines using the primers in T38964-
CC   T39005. To confirm the identity of amplified cDNA, digoxigenin-
CC   labelled probes specific for each cytokine (see T39006-T39021)
CC   were hybridised with Southern blots of amplified sequences. The
CC   expression profile for regressing and non-regressing warts was
CC   established and compared to cytokine expression patterns in normal
CC   cervical tissue. Results showed that interleukin 12 is barely
CC   expressed (if at all) in non-regressing warts, but is expressed in
CC   regressing warts. This suggests a central role for IL-12 in wart
CC   regression. It has been found that IL-12 can be used (especially
CC   as a vaccine adjuvant) for treating papilloma virus-associated
CC   lesions such as condyloma acuminata (anogenital warts) caused by
CC   human papilloma virus type 6 (HPV-6) and/or HPV-11 and more
CC   generally for treatment of tumours associated with HPV16 and HPV18
CC   infection e.g. anogenital, cutaneous, laryngeal and oesophageal
CC   cancers.
SQ   Sequence   29 BP;    7 A;    6 C;    9 G;    7 T;

  Query Match           51.9%;  Score 14;  DB 29;  Length 29;
  Best Local Similarity 85.0%;  Pred. No. 1.94e+02;
  Matches    17;  Conservative    0;  Mismatches   3;  Indels   0;  Gaps   0;

Db       2 agatcgcgaggctcaaagtc 21
           ||| |  |||||||||||||
Cp      23 AGACCCTGAGGCTCAAAGTC 4


RESULT   20
ID   Q08506 standard; DNA; 21 BP.
AC   Q08506;
DT   29-MAR-1992  (first entry)
DE   Sequence of 3' probe, corresponding to a region encoding amino
DE   acids 123-130 of the mature protein of human interleukin-3
DE   (huIL-3).
KW   Lymphokine; bone marrow proliferation; cytopenia therapy; ss.
OS   Homo sapiens.
PN   WO9001039-A.
PD   08-FEB-1990.
PF   14-JUN-1989; U02599.
PR   20-JUL-1988; US-221699.
PA   (IMMU-) IMMUNEX CORP.
PI   Anderson DM, Cosman DJ, Price VL;
DR   WPI; 90-067162/09.
PT   Compsns. contg. recombinant non-glycosylated human interleukin-3
PT   - has increased biological activity and binding affinity, for
PT   treating cytopenias
PS   Example; Page 10; 23pp; English.
CC   The inventors claim a pharmaceutical compsn. which contains an
CC   effective amt. of a recombinant human interleukin-3 protein analogue,
CC   rhuIL-3, (Asp15,Asp70). The rhuIL-3 analogue has AA SQ in R09326.
CC   The compsn. may also comprise the N-terminal octapeptide in R09327,
CC   and a diluent and 1 or more than 1 biological response modifier.
CC   The compsn. has a biological specific activity of equal to or more
CC   than 4.0 x 10 to the 7 mcg/mg in a human bone marrow proliferation
CC   assay, and a binding affinity for human monocyte IL-3 receptors of
CC   equal to or more than 4.0 x 10 to the 10 (M to the minus 1).
SQ   Sequence   21 BP;    5 A;    5 C;    7 G;    4 T;

  Query Match           48.1%;  Score 13;  DB 3;  Length 21;
  Best Local Similarity 100.0%;  Pred. No. 5.64e+02;
  Matches    13;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db       7 gaggctcaaagtc 19
           |||||||||||||
Cp      16 GAGGCTCAAAGTC 4


RESULT   21
ID   Q10345 standard; DNA; 21 BP.
AC   Q10345;
DT   10-APR-1991  (first entry)
DE   Probe to the human interleukin-3 gene.
KW   huIL-3; urticaria; granulopoiesis; erythropoiesis; thrombopoiesis;
KW   neutropaenia; anaemia; thrombocytopaenia; ss.
OS   Homo sapiens.
PN   WO9100350-A.
PD   10-JAN-1991.
PF   13-JUN-1990; U03345.
PR   30-JUN-1989; US-374667.
PA   (IMMU-) IMMUNEX CORP.
PI   Urdal DL, Sassenfeld H;
DR   WPI; 91-036745/05.
PT   Non-glycosylated human interleukin-3 analog proteins - expressed
PT   by transformed yeast of Saccharomyces cerevisiae which do not
PT   give detectable urticaria
PS   Example A; Page 7; 18pp; English.
CC   Probes were used in the isolation of human IL-3, which was then
CC   expressed in a modified form, with a mutation in the
CC   N-glycosylation sites. The modified IL-3 does not result in
CC   ulticaria or infiltration of mast cells and lymphocytes into the
CC   dermis. It stimmaltes granulopoiesis, erythropoiesis and
CC   thrombopoiesis in vivo and may used to treat neutropaenia, anaemia
CC   and thrombocytopaenia.
SQ   Sequence   21 BP;    5 A;    5 C;    7 G;    4 T;

  Query Match           48.1%;  Score 13;  DB 2;  Length 21;
  Best Local Similarity 100.0%;  Pred. No. 5.64e+02;
  Matches    13;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db       7 gaggctcaaagtc 19
           |||||||||||||
Cp      16 GAGGCTCAAAGTC 4
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RESULT   22
ID   Q42804 standard; cDNA; 21 BP.
AC   Q42804;
DT   15-SEP-1993  (first entry)
DE   Human IL-3 probe.
KW   Mast cell growth factor; interleukin; haematopoietic progenitor cell;
KW   bone marrow cell; proliferation; differentiation; functional activation;
KW   peripheral blood leukocyte; circulating granulocyte; ss.
OS   Synthetic.
PN   WO9310229-A.
PD   27-MAY-1993.
PF   19-NOV-1992; U09848.
PR   22-NOV-1991; US-797553.
PA   (IMMV ) IMMUNEX CORP.
PI   Williams DE;
DR   WPI; 93-182546/22.
PT   MGF-interleukin-3 fusion proteins having enhanced activity - used
PT   for regulating immune and inflammatory responses
PS   Example 1; Page 17; 41pp; English.
CC   Two oligonucleotides were synthesised, with sequences complementary
CC   to selected 5' and 3' sequences of the huIL-3 gene.  The 5' probe,
CC   complementary to a sequence encoding part of the huIL-3 leader, has
CC   the sequence given in Q42803.  The 3' probe, corresp. to a region
CC   encoding amino acids 123-130 of the mature protein, has the
CC   sequence given in Q42804.
SQ   Sequence   21 BP;    5 A;    5 C;    7 G;    4 T;

  Query Match           48.1%;  Score 13;  DB 7;  Length 21;
  Best Local Similarity 100.0%;  Pred. No. 5.64e+02;
  Matches   13;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db       7 gaggctcaaagtc 19
           |||||||||||||
Cp      16 GAGGCTCAAAGTC 4


RESULT   23
ID   T63590 standard; DNA; 22 BP.
AC   T63590;
DT   01-JUL-1997  (first entry)
DE   CD59 PCR primer used to screen human genomic DNA library.
KW   Xenotransplantation; organ transplant; transgenic animal;
KW   transgenic pig; transgenic mouse; antibody mediated rejection;
KW   hyperacute rejection; CD59; complement inhibitor; primer; PCR;
KW   polymerase chain reaction; bacteriophage P1; ss.
OS   Synthetic.
PN   WO9712035-A2.
PD   03-APR-1997.
PF   23-SEP-1996; U15255.
PR   27-SEP-1995; US-004461.
PR   03-JUL-1996; US-675773.
PA   (NEXT-) NEXTRAN.
PI   Byrne GW,  Diamond LE,  Logan JS,  Sharma A;
DR   WPI; 97-225881/20.
PT   Transgenic animals expressing antigen reducing enzyme and complement
PT   inhibitor  - used for production of materials suitable for human
PT   transplantation having a reduced risk of rejection
PS   Example 4.1; Page 107; 146pp; English.
CC   Oligonucleotide pairs (T63589-98), designed from previously
CC   published sequence data and corresponding to the 5' and 3' regions
CC   of CD59, CD46 and CD55 genes, were used to screen, by PCR, a human
CC   genomic library constructed in phage P1.  The primer pair given in
CC   T63589-90 yielded a 288 bp product located 1602 bp 5' of the
CC   transcriptional start of the CD59 gene.  Transgenic mouse and pig
CC   lines contg. selected P1 clones were produced.  Expression of
CC   complement inhibitors such as CD59, CD46 (membrane cofactor
CC   protein) and CD55 (decay accelerating factor) in the endothelial
CC   cells of transgenic animals can generate material suitable for
CC   transplantation to humans, suppressing complement activation and
CC   thereby reducing immune reaction.
SQ   Sequence   22 BP;    5 A;    4 C;    8 G;    5 T;

  Query Match           48.1%;  Score 13;  DB 29;  Length 22;
  Best Local Similarity 58.8%;  Pred. No. 5.64e+02;
  Matches   10;  Conservative    5;  Mismatches   2;  Indels   0;  Gaps   0;

Db       5 actttgagggtcagggt 21
           ||:::|||  :|||||:
Qy       5 ACUUUGAGCCUCAGGGU 21


RESULT   24
ID   V42514 standard; DNA; 24 BP.
AC   V42514;
DT   05-OCT-1998  (first entry)
DE   PCR primer used to amplify the basic region and helix II DNA of RELAX.
KW   Basic helix-loop-helix; BHLH; RELAX; Rat Embryonic Longitudinal Axis;
KW   control; gene expression; transcriptional activator; targeting;
KW   protein expression; central nervous system; CNS; treatment;
KW   nervous system disorder; PCR primer; ss.
OS   Synthetic.
OS   Rattus sp.
PN   WO9827206-A2.
PD   25-JUN-1998.
PF   19-DEC-1997; F07368.
PR   19-DEC-1996; FR-015651.
PA   (RHON ) RHONE-POULENC RORER SA.
PI   Mallet J, Ravassard P, Icard-Liepkalns C;
DR   WPI; 98-362775/31.
PT   Basic helix-loop-helix polypeptide and related nucleic acid - with
PT   transcriptional activity, for targeting expression of genes to
PT   central nervous system and treatment of nervous disease
PS   Example 1; Page 10; 28pp; French.
CC   PCR primers V42513-14 are degenerate primers used to amplify DNA encoding
CC   the basic domain and helix II of a basic helix-loop-helix (BHLH) type
CC   protein, designated RELAX (Rat Embryonic Longitudinal Axis) protein.
CC   The protein is used to control and  participate in gene expression,
CC   by acting as transcriptional activator, strictly dependent on the
CC   presence of an intact E box (CANNTG), particularly for targeting
CC   expression of proteins to the central nervous system (CNS). The
CC   nucleic acid sequence can be used to treat nervous system disorders,
CC   and antisense sequences can be used to control mRNA transcription.
SQ   Sequence   24 BP;    2 A;    3 C;    6 G;    5 T;

  Query Match           48.1%;  Score 13;  DB 46;  Length 24;
  Best Local Similarity 33.3%;  Pred. No. 5.64e+02;
  Matches    5;  Conservative    9;  Mismatches   1;  Indels   0;  Gaps   0;

Db       4 srdtytcagggtsyb 18
           ::: ::|||||::::
Qy      10 GAGCCUCAGGGUCUG 24


RESULT   25
ID   V95538 standard; RNA; 27 BP.
AC   V95538;
DT   24-FEB-1999  (first entry)
DE   Human c-fos hammerhead ribozyme nucleotide position 1267.
KW   Human; c-fos; hammerhead ribozyme; hairpin ribozyme; target site;
KW   cancer; oncogene; leukaemia; neuroblastoma; diagnosis; genetic drift;
KW   mutation; diseased cell; ss.
OS   Synthetic.
OS   Homo sapiens.
PN   WO9832846-A2.
PD   30-JUL-1998.
PF   20-JAN-1998; U01017.
PR   23-JAN-1997; US-037658.
PA   (RIBO-) RIBOZYME PHARM INC.
PI   Jarvis T, McSwiggen JA, Stinchcomb DT;
DR   WPI; 98-427942/36.
PT   Enzymatic nucleic acid molecules which specifically cleave RNA
PT   derived from a c-fos gene - useful for treating conditions related
PT   to levels of c-fos, especially cancer
PS   Claim 9; Page 52; 72pp; English.
CC   The present invention describes an enzymatic nucleic acid molecule which
CC   specifically cleaves RNA derived from a c-fos gene. V95401 to V95540
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CC   and V95541 to V95584 represent hammerhead ribozymes and hairpin
CC   ribozymes, respectively, which specifically cleave human c-fos. V95261
CC   to V95400 and V95585 to V95628 represent human c-fos target sequences.
CC   The enzymatic nucleic acid molecules can be used for treating cancer
CC   associated with elevated levels of c-fos oncogene, especially
CC   leukaemias, neuroblastomas and lung, breast and colon cancers. The
CC   ribozymes may also be used as diagnostic tools to examine genetic drift
CC   and mutations within diseased cells, or to detect the presence of c-fos
CC   RNA in a cell.
SQ   Sequence   27 BP;    9 A;    4 C;    9 G;    4 U;

  Query Match           48.1%;  Score 13;  DB 54;  Length 27;
  Best Local Similarity  68.2%;  Pred. No. 5.64e+02;
  Matches   15;  Conservative    2;  Mismatches   5;  Indels   0;  Gaps   0;

Db       5 gagccugaugangaaagucaga 26
           || ||:|| |   ||||:||||
Cp      22 GACCCTGAGGCTCAAAGTCAGA 1


RESULT   26
ID   Q28596 standard; DNA; 29 BP.
AC   Q28596;
DT   23-FEB-1993  (first entry)
DE   HLA DPA1 primer #513.
KW   Biotin; primer; [35S]-alpha-thio-dNTP; radioactive label;
KW   primer extension; template-directed; sequence-specific labelling;
KW   DNA polymerase-catalysed extension; primer-template complex; ss.
OS   Synthetic.
PN   WO9215712-A.
PD   17-SEP-1992.
PF   04-MAR-1992; U01905.
PR   05-MAR-1991; US-664837.
PR   11-OCT-1991; US-775786.
PA   (MOLE-) MOLECULAR TOOL INC.
PI   Anderson S, Goelet P, Knapp MR;
DR   WPI; 92-331756/40.
PT   Nucleic acid template-dependent, primer extension reaction -
PT   using at least two different sequence terminators, for genetic
PT   typing
PS   Disclosure; Fig 10; 78pp; English.
CC   The sequences given in Q28578-98 are primers which were used to
CC   illustrate the methods of the invention.  The methods use a reagent
CC   composition comprising an aqueous carrier and an admixture of at least
CC   two different terminators of a nucleic acid template-dependant, primer
CC   extension reaction.  Each terminator is capable of specifically
CC   terminating the reaction in a manner strictly dependant in the
CC   identity of the unpaired nucleotide base immediatly adjacent to, and
CC   downstream of the 3' end of the primer.  At least one of the
CC   terminators is labelled with a detectable marker eg. 35S.  The
CC   methods allow analyses of nucleic acid sequences that can be useful in
CC   the diagnosis of infectious dieases, genetic disorders and the
CC   identification of individuals and their parentage.  See also
CC   Q28575-77.
SQ   Sequence   29 BP;    8 A;    11 C;    7 G;    3 T;

  Query Match           48.1%;  Score 13;  DB 5;  Length 29;
  Best Local Similarity  93.3%;  Pred. No. 5.64e+02;
  Matches   14;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db       5 ccctgagcctcaaag 19
           ||||||| |||||||
Cp      20 CCCTGAGGCTCAAAG 6


RESULT   27
ID   T47213 standard; DNA; 33 BP.
AC   T47213;
DT   01-SEP-1997  (first entry)
DE   PCR primer for plasmid pPLMuIL72.
KW   Human; interleukin 1; beta; receptor; IL72; antagonist; hybrid;
KW   fusion; polymerase chain reaction; PCR; amplification; plasmid;
KW   pPLMuIL72; ss.
OS   Synthetic.
PN   WO9639503-A1.
PD   12-DEC-1996.
PF   04-JUN-1996; E08422.
PR   05-JUN-1995; US-463377.
PR   05-JUN-1995; US-462648.
PR   05-JUN-1995; US-463224.
PA   (CIBA ) CIBA GEIGY AG.
PI   Schmitz A,  Van Heeke G,  Van Oostrum J;
DR   WPI; 97-043125/04.
PT   New human complement C5a poly-peptide derivs. - used as C5a receptor
PT   antagonists, partic. for treating C5a-mediated diseases and
PT   inflammatory conditions
PS   Example 17; Page 46; 93pp; English.
CC   The present sequence is a primer for the PCR amplification of the
CC   plasmid pPLMuIL72, which contains the DNA sequence of IL72 flanked
CC   by NcoI and GamHI restriction sites. IL72 is a hybrid protein
CC   composed of human interleukin 1 beta and human interleukin 1
CC   receptor antagonist.
SQ   Sequence   33 BP;    11 A;    6 C;    9 G;    7 T;

  Query Match           48.1%;  Score 13;  DB 31;  Length 33;
  Best Local Similarity  88.2%;  Pred. No. 5.64e+02;
  Matches   15;  Conservative    0;  Mismatches   2;  Indels   0;  Gaps   0;

Db      12 cagagcatgaggctcaa 28
           |||| | |||||||||||
Cp      24 CAGACCCTGAGGCTCAA 8


RESULT   28
ID   T70502 standard; DNA; 42 BP.
AC   T70502;
DT   06-MAR-1998  (first entry)
DE   Human Immunoglobulin D segment probe DXP4.
KW   Immunoglobulin heavy chain; heterologous antibody; transgene; probe;
KW   monoclonal antibody; immunogenicity; diversity segment; D segment; ss.
OS   Synthetic.
OS   Homo sapiens.
PN   US5633425-A.
PD   27-MAY-1997.
PF   05-FEB-1992; 834539.
PR   29-AUG-1990; US-574448.
PR   31-AUG-1990; US-575962.
PA   (GENP-) GENPHARM INT INC.
PI   Kay RM,  Lonberg N;
DR   WPI; 97-297410/27.
PT   Transgenic mouse for heterologous antibody production - containing
PT   DNA encoding human immunoglobulin components
PS   Example 5; Column 35; 90pp; English.
CC   This oligonucleotide was used as a probe to facilitate in the cloning of
CC   the D segment from a human immunoglobulin. Probe DXP4 isolated a 3.2 kb
CC   XhoI fragment containing a D segment which is used in a novel method of
CC   developing transgenic non-human animals capable of producing heterologous
CC   antibodies encoded by human immunoglobulin genes. Such transgenically
CC   produced monoclonal antibodies should alleviate the intrinsic
CC   immunogenicity of non-human immunoglobulins allowing the development of
CC   new in vivo applications.
SQ   Sequence   42 BP;    10 A;    11 C;    15 G;    6 T;

  Query Match           48.1%;  Score 13;  DB 36;  Length 42;
  Best Local Similarity  68.4%;  Pred. No. 5.64e+02;
  Matches   13;  Conservative    3;  Mismatches   3;  Indels   0;  Gaps   0;

Db       3 ctgaaatggagcctcaggg 21
           |:||  : ||||||:||||||
Qy       2 CUGACUUUGAGCCUCAGGG 20


RESULT   29
ID   Q23427 standard; DNA; 42 BP.
AC   Q23427;
DT   30-JUL-1992  (first entry)
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DE Probe for human D segments - DXP4.
KW Rat; constant region; immunoglobulin; ss.
OS Synthetic.
PN WO9203918-A.
PD 19-MAR-1992.
PF 28-AUG-1991; U06185.
PR 29-AUG-1990; US-574748.
PR 31-AUG-1990; US-575962.
PA (GENP-) GENPHARM INT INC.
PI Lonberg N, Kay R;
DR WPI; 92-113962/14.
PT Immunoglobulin trans:genes - for prodn. of heterologous
PT non-rearranged and/or rearranged Ig chains
PS Example 5; Page 59; 172pp; English.
CC The probe was used to isolate phage clones contg. D segments from a
CC human genomic library. The probe, along with probe DXP1 and DN4
CC (Q23426,8) are specific for for diversity region sequences
CC (Y. Ichihara, et al., (1988), EMBO J., 7: 4141-4150).
CC See also Q23419-50 and Q22417-30.
SQ Sequence 42 BP; 10 A; 11 C; 15 G; 6 T;

Query Match 48.1%; Score 13; DB 3; Length 42;
Best Local Similarity 68.4%; Pred. No. 5.64e+02;
Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

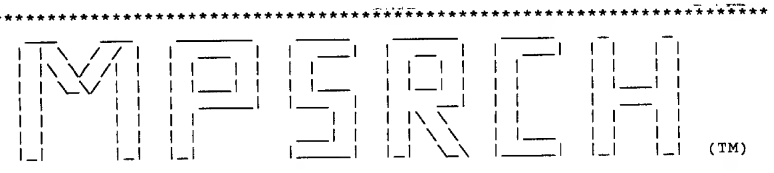
Db 3 ctgaaatggagcctcaggg 21
|:|| : |||||:|||||
Qy 2 CUGACUUUGAGCCUCAGGG 20

RESULT 30
ID V12519 standard; DNA; 42 BP.
AC V12519;
DT 26-MAY-1998 (first entry)
DE Probe DXP4 for human D segment.
KW Transgenic mouse; human; immunoglobulin; heavy chain segment; J region;
KW joining region; constant region; VH family; variable gene; gamma isotype;
KW diversity gene; isotype switching sequence; mu isotype; Ig production;
KW monoclonal antibody; MAb production; antigen; heavy chain isotype;
KW antigenic stimulation; probe; ss.
OS Synthetic.
OS Homo sapiens.
PN US5625126-A.
PD 29-APR-1997.
PF 07-DEC-1994; 352322.
PR 07-DEC-1994; US-352322.
PR 29-AUG-1990; US-574748.
PR 31-AUG-1990; US-575962.
PR 17-DEC-1991; US-810279.
PR 05-FEB-1992; US-834539.
PR 18-MAR-1992; US-853408.
PR 23-JUN-1992; US-904068.
PR 16-DEC-1992; US-990860.
PR 26-APR-1993; US-053131.
PR 22-JUL-1993; US-096762.
PR 18-NOV-1993; US-155301.
PR 03-DEC-1993; US-161739.
PR 10-DEC-1993; US-165699.
PR 09-MAR-1994; US-209741.
PA (GENP-) GENPHARM INT INC.
PI Kay RM, Lonberg N;
DR WPI; 97-258277/23.
PT Human antibody producing transgenic mouse - containing transgene
PT comprising human V, D and J genes and sequences to provide isotype
PT switching in lymphocytes
PS Example 4; Column 52; 153pp; English.
CC This sequence represents a probe for the human diversity (D) segments.
CC The identified sequence sequence is used in the plasmid pRE3, which is
CC used to develop the transgenic mouse of the invention. The transgenic
CC mouse of the invention contains in its genome a transgene comprising in
CC operable linkage human variable (V), diversity (D) and J genes, a human
CC mu constant region gene (muCH), at least 2 different non-mu human CH
CC genes and associated isotype switching sequences, where human mu and
CC gamma switch sequences are located in closer proximity to each other than
CC in the naturally occurring human immunoglobulin (Ig) locus, and where in
CC lymphocytes of the mouse the transgene undergoes productive VDJ
CC rearrangement and mu to gamma isotype switching by recombination between
CC the human mu and gamma sequences, so that the mouse produces a serum
CC containing Ig of at least 3 human heavy chain isotypes in response to
CC antigenic stimulation. The transgenic mice can be used to produce human
CC Ig and monoclonal antibodies (MAb), which are specifically reactive with
CC human antigens. The MAb can be used in therapeutic or diagnostic
CC applications. The transgenic mice can produce human MAb of multiple
CC isotypes by undergoing isotype switching.
SQ Sequence 42 BP; 10 A; 11 C; 15 G; 6 T;

Query Match 48.1%; Score 13; DB 39; Length 42;
Best Local Similarity 68.4%; Pred. No. 5.64e+02;
Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db 3 ctgaaatggagcctcaggg 21
|:|| : |||||:|||||
Qy 2 CUGACUUUGAGCCUCAGGG 20

Search completed: Mon Aug 2 12:00:55 1999
Job time : 264 secs.



MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Mon Aug 2 12:04:54 1999; MasPar time 5.00 Seconds
383.026 Million cell updates/sec

Tabular output not generated.

Title: >US-09-121-239-23
Description: (1-27) from US09121239.seq
Perfect Score: 27
N.A. Sequence: 1 UCUGACUUUGAGCCUCAGGGUCUGAGU 27
Comp: AGACTGAAACTCGGAGTCCCAGACTCA

Scoring table: TABLE default
Gap 10

Nmatch STD : Dbase 0; Query 0

Searched: 137068 seqs, 35432894 bases x 2

Post-processing: Minimum Match 0%
Listing first 1000 summaries
Maximum DB seq length 50

Database: n-issued
1:5A_COMB 2:5B_COMB 3:5C_COMB 4:PCT9_COMB 5:backfiles1

Statistics: Mean 5.285; Variance 3.144; scale 1.681

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
c	1	22	81.5	22	4	PCT-US94-0	Sequence 10, Applicati	2.20e-03
c	2	22	81.5	22	4	PCT-US94-0	Sequence 1, Applicatio	2.20e-03
c	3	22	81.5	22	2	US-08-525-	Sequence 1, Applicatio	2.20e-03
c	4	22	81.5	22	1	US-08-013-	Sequence 1, Applicatio	2.20e-03
c	5	22	81.5	22	1	US-08-122-	Sequence 10, Applicati	2.20e-03
c	6	15	55.6	20	1	US-07-872-	Sequence 13, Applicati	1.56e+01
c	7	15	55.6	20	3	US-08-761-	Sequence 7, Applicatio	1.56e+01
	8	15	55.6	40	3	US-08-761-	Sequence 2, Applicatio	1.56e+01
	9	15	55.6	40	3	US-08-761-	Sequence 1, Applicatio	1.56e+01
c	10	13	48.1	27	4	PCT-US95-1	Sequence 13, Applicati	1.55e+02
c	11	13	48.1	33	3	US-08-463-	Sequence 61, Applicati	1.55e+02
	12	13	48.1	42	2	US-08-645-	Sequence 25, Applicati	1.55e+02
	13	13	48.1	42	2	US-08-053-	Sequence 25, Applicati	1.55e+02
	14	13	48.1	42	3	US-08-096-	Sequence 25, Applicati	1.55e+02
	15	13	48.1	42	4	PCT-US92-0	Sequence 17, Applicati	1.55e+02
	16	13	48.1	42	1	US-07-834-	Sequence 17, Applicati	1.55e+02
	17	13	48.1	42	4	PCT-US92-1	Sequence 25, Applicati	1.55e+02
	18	13	48.1	42	3	US-07-853-	Sequence 25, Applicati	1.55e+02
	19	13	48.1	45	3	US-08-399-	Sequence 53, Applicati	1.55e+02
	20	12	44.4	26	4	PCT-US96-0	Sequence 269, Applicat	4.61e+02
	21	12	44.4	37	3	US-08-428-	Sequence 39, Applicati	4.61e+02
c	22	12	44.4	37	3	US-08-428-	Sequence 7, Applicatio	4.61e+02
c	23	12	44.4	37	3	US-08-428-	Sequence 38, Applicati	4.61e+02
c	24	11	40.7	24	4	PCT-US95-0	Sequence 19, Applicati	1.31e+03
c	25	11	40.7	25	1	US-07-999-	Sequence 20, Applicati	1.31e+03
c	26	11	40.7	27	3	US-08-758-	Sequence 426, Applicat	1.31e+03
	27	11	40.7	29	4	PCT-US95-0	Sequence 62, Applicati	1.31e+03
	28	11	40.7	31	1	US-08-476-	Sequence 29, Applicati	1.31e+03
c	29	11	40.7	31	3	US-08-483-	Sequence 7, Applicatio	1.31e+03
c	30	11	40.7	31	1	US-08-314-	Sequence 7, Applicatio	1.31e+03
c	31	11	40.7	31	3	US-08-482-	Sequence 7, Applicatio	1.31e+03
	32	11	40.7	32	1	US-08-197-	Sequence 4, Applicatio	1.31e+03
	33	11	40.7	35	4	PCT-US94-0	Sequence 18, Applicati	1.31e+03
c	34	11	40.7	36	1	US-07-917-	Sequence 19, Applicati	1.31e+03
c	35	11	40.7	42	4	PCT-US92-0	Sequence 15, Applicati	1.31e+03
	36	11	40.7	47	5	5284931-19	Patent No. 5284931.	1.31e+03
c	37	11	40.7	48	2	US-08-645-	Sequence 23, Applicati	1.31e+03
c	38	11	40.7	50	1	US-07-994-	Sequence 25, Applicati	1.31e+03
c	39	11	40.7	50	4	PCT-US93-1	Sequence 456, Applicat	1.31e+03

Note: Post-processor removed 961 summaries from list due to search parameters chosen.

ALIGNMENTS

RESULT 1
ID PCT-US94-09963A-10 STANDARD; DNA; UNC; 22 BP.
AC XXXXXX
DT
DE Sequence 10, Application PC/TUS9409963A
CC Sequence 10, Application PC/TUS9409963A
CC GENERAL INFORMATION:
CC TITLE OF INVENTION: MULTI-UNIT RIBOZYME
CC TITLE OF INVENTION: INHIBITION OF ONCOGENE EXPRESSION
CC NUMBER OF SEQUENCES: 11
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Seidel, Gonda, Lavorgna
CC ADDRESSEE: & Monaco, P.C.
CC STREET: Two Penn Center Plaza, Suite 1800
CC CITY: Philadelphia
CC STATE: Pennsylvania
CC COUNTRY: U.S.A.
CC ZIP: 19102
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
CC COMPUTER: IBM PS/2
CC OPERATING SYSTEM: MS-DOS
CC SOFTWARE: WordPerfect 5.1
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US94/09963A
CC FILING DATE:
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 122,795
CC FILING DATE: 15 September 1993
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Monaco, Daniel A.
CC REGISTRATION NUMBER: 30,480
CC REFERENCE/DOCKET NUMBER: 6056-192
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (215) 568-8383
CC TELEFAX: (215) 568-5549
CC TELEX: None
CC INFORMATION FOR SEQ ID NO: 10:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 22 Nucleotides
CC TYPE: nucleic acid
CC STRANDEDNESS: single stranded
CC TOPOLOGY: linear
SQ SEQUENCE 22 BP; 6 A; 7 C; 5 G; 4 T; 0 OTHER.

Query Match 81.5%; Score 22; DB 4; Length 22;

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  Best Local Similarity 100.0%;  Pred. No. 2.20e-03;
  Matches   22;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db       1 TCAGACCCTGAGGCTCAAAGTC 22
           ||||||||||||||||||||||
Cp      25 TCAGACCCTGAGGCTCAAAGTC 4


RESULT    2
ID   PCT-US94-00680-1 STANDARD; DNA; UNC; 22 BP.
AC   xxxxxx
DT
DE   Sequence 1, Application PC/TUS9400680
CC   Sequence 1, Application PC/TUS9400680
CC    GENERAL INFORMATION:
CC      APPLICANT:  University of Iowa, Research Foundation
CC      TITLE OF INVENTION:  Quarternary Amine Surfactants and
CC      TITLE OF INVENTION:  Methods of Using Same in Isolation of RNA
CC      NUMBER OF SEQUENCES:  2
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Howson and Howson
CC        STREET:  Spring House Corporate Cntr, PO Box 457
CC        CITY:  Spring House
CC        STATE:  Pennsylvania
CC        COUNTRY:  USA
CC        ZIP:  19477
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, Version #1.25
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  PCT/US94/00680
CC        FILING DATE:
CC        CLASSIFICATION:
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  US 08/013,419
CC        FILING DATE:  01-FEB-1993
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  US 08/113,727
CC        FILING DATE:  27-AUG-1993
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Bak, Mary E.
CC        REGISTRATION NUMBER:  31,215
CC        REFERENCE/DOCKET NUMBER:  UIRF1APCT
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  215-540-9200
CC        TELEFAX:  215-540-5818
CC    INFORMATION FOR SEQ ID NO:  1:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  22 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  single
CC        TOPOLOGY:  unknown
CC      MOLECULE TYPE:  DNA (genomic)
SQ   SEQUENCE 22 BP; 6 A; 7 C; 5 G; 4 T; 0 OTHER.

  Query Match           81.5%;  Score 22;  DB 4;  Length 22;
  Best Local Similarity 100.0%;  Pred. No. 2.20e-03;
  Matches   22;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db       1 TCAGACCCTGAGGCTCAAAGTC 22
           ||||||||||||||||||||||
Cp      25 TCAGACCCTGAGGCTCAAAGTC 4


RESULT    3
ID   US-08-525-818-1 STANDARD; DNA; UNC; 22 BP.
AC   xxxxxx
DT
DE   Sequence 1, Application US/08525818
CC   Sequence 1, Application US/08525818
CC   Patent No. 5728822
CC    GENERAL INFORMATION:
CC      APPLICANT:  Macfarlane, Donald E.
CC      TITLE OF INVENTION:  Quaternary Amine Surfactants and Methods
CC      TITLE OF INVENTION:  of Using Same in Isolation of RNA
CC      NUMBER OF SEQUENCES:  2
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Howson and Howson
CC        STREET:  Spring House Corporate Cntr., P.O. Box 457
CC        CITY:  Spring House
CC        STATE:  Pennsylvania
CC        COUNTRY:  USA
CC        ZIP:  19477
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, Version #1.25
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/525,818
CC        FILING DATE:
CC        CLASSIFICATION:  536
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/113,727
CC        FILING DATE:
CC        APPLICATION NUMBER:  US 08/013,419
CC        FILING DATE:  01-FEB-1993
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Bak, Mary E.
CC        REGISTRATION NUMBER:  31,215
CC        REFERENCE/DOCKET NUMBER:  UIRF1AUSA
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  215-540-9200
CC        TELEFAX:  215-540-5818
CC    INFORMATION FOR SEQ ID NO:  1:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  22 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  single
CC        TOPOLOGY:  unknown
CC      MOLECULE TYPE:  DNA (genomic)
SQ   SEQUENCE 22 BP; 6 A; 7 C; 5 G; 4 T; 0 OTHER.

  Query Match           81.5%;  Score 22;  DB 2;  Length 22;
  Best Local Similarity 100.0%;  Pred. No. 2.20e-03;
  Matches   22;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db       1 TCAGACCCTGAGGCTCAAAGTC 22
           ||||||||||||||||||||||
Cp      25 TCAGACCCTGAGGCTCAAAGTC 4


RESULT    4
ID   US-08-013-419-1 STANDARD; DNA; UNC; 22 BP.
AC   xxxxxx
DT
DE   Sequence 1, Application US/08013419
CC   Sequence 1, Application US/08013419
CC   Patent No. 5300635
CC    GENERAL INFORMATION:
CC      APPLICANT:  Macfarlane, Donald E.
CC      TITLE OF INVENTION:  Product and Process for Isolating RNA
CC      NUMBER OF SEQUENCES:  2
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Howson and Howson
CC        STREET:  Spring House Corporate Center, P.O. Box 457
CC        CITY:  Spring House
CC        STATE:  Pennsylvania
CC        COUNTRY:  USA
CC        ZIP:  19477
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
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CC        SOFTWARE:  PatentIn Release #1.0, Version #1.25
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/013,419
CC        FILING DATE:  19930201
CC        CLASSIFICATION:  435
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Bak, Mary E.
CC        REGISTRATION NUMBER:  31,215
CC        REFERENCE/DOCKET NUMBER:  URIF1USA
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  215-540-9206
CC        TELEFAX:  215-540-5818
CC    INFORMATION FOR SEQ ID NO:  1:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  22 base pairs
CC        TYPE:  NUCLEIC ACID
CC        STRANDEDNESS:  unknown
CC        TOPOLOGY:  unknown
CC      MOLECULE TYPE:  DNA (genomic)
SQ   SEQUENCE 22 BP; 6 A; 7 C; 5 G; 4 T; 0 OTHER.

  Query Match           81.5%;  Score 22;  DB 1;  Length 22;
  Best Local Similarity 100.0%;  Pred. No. 2.20e-03;
  Matches   22;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db      1 TCAGACCCTGAGGCTCAAAGTC 22
          ||||||||||||||||||||||
Cp     25 TCAGACCCTGAGGCTCAAAGTC 4


RESULT    5
ID   US-08-122-795B-10 STANDARD; DNA; UNC; 22 BP.
AC   xxxxxx
DT
DE   Sequence 10, Application US/08122795B
CC   Sequence 10, Application US/08122795B
CC   Patent No. 5635385
CC    GENERAL INFORMATION:
CC      APPLICANT:  Lance H. Leopold
CC      APPLICANT:  Scott K. Shore
CC      APPLICANT:  Moole V. R. Reddy
CC      APPLICANT:  E. Premkumar Reddy
CC      TITLE OF INVENTION:  MULTI-UNIT RIBOZYME
CC      TITLE OF INVENTION:  INHIBITION OF ONCOGENE EXPRESSION
CC      NUMBER OF SEQUENCES:  11
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Seidel, Gonda, Lavorgna
CC        ADDRESSEE:  & Monaco, P.C.
CC        STREET:  Two Penn Center Plaza, Suite 1800
CC        CITY:  Philadelphia
CC        STATE:  Pennsylvania
CC        COUNTRY:  U.S.A.
CC        ZIP:  19102
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Diskette, 3.50 inch, 720 Kb
CC        COMPUTER:  IBM PS/2
CC        OPERATING SYSTEM:  MS-DOS
CC        SOFTWARE:  WordPerfect 5.1
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/122,795B
CC        FILING DATE:
CC        CLASSIFICATION:  514
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  122,795
CC        FILING DATE:  15 September 1993
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Monaco, Daniel A.
CC        REGISTRATION NUMBER:  30,480
CC        REFERENCE/DOCKET NUMBER:  6056-192
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  (215) 568-8383
CC        TELEFAX:  (215) 568-5549
CC        TELEX:  No. 5635385e
CC    INFORMATION FOR SEQ ID NO:  10:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  22 Nucleotides
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  single stranded
CC        TOPOLOGY:  linear
SQ   SEQUENCE 22 BP; 6 A; 7 C; 5 G; 4 T; 0 OTHER.

  Query Match           81.5%;  Score 22;  DB 1;  Length 22;
  Best Local Similarity 100.0%;  Pred. No. 2.20e-03;
  Matches   22;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db      1 TCAGACCCTGAGGCTCAAAGTC 22
          ||||||||||||||||||||||
Cp     25 TCAGACCCTGAGGCTCAAAGTC 4


RESULT    6
ID   US-07-872-678A-13 STANDARD; DNA; UNC; 20 BP.
AC   xxxxxx
DT
DE   Sequence 13, Application US/07872678A
CC   Sequence 13, Application US/07872678A
CC   Patent No. 5541060
CC    GENERAL INFORMATION:
CC      APPLICANT:  Bell, Graeme, et al.
CC      TITLE OF INVENTION:  DETECTION OF EARLY-ONSET
CC      TITLE OF INVENTION:  NON-INSULIN-DEPENDENT DIABETES MELLITUS
CC      NUMBER OF SEQUENCES:  48
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Arnold, White & Durkee
CC        STREET:  Post Office Box 4433
CC        CITY:  Houston
CC        STATE:  Texas
CC        COUNTRY:  USA
CC        ZIP:  77210
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, Version #1.25
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/07/872,678A
CC        FILING DATE:  22-APRIL-1992
CC        CLASSIFICATION:  435
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Coughlin, Daniel F.
CC        REGISTRATION NUMBER:  36,111
CC        REFERENCE/DOCKET NUMBER:  ARCD016
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  713-787-1400
CC        TELEFAX:  713-789-2679
CC        TELEX:  79-0924
CC    INFORMATION FOR SEQ ID NO:  13:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  20 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  single
CC        TOPOLOGY:  linear
CC      MOLECULE TYPE:  DNA ( genomic)
SQ   SEQUENCE 20 BP; 6 A; 5 C; 4 G; 5 T; 0 OTHER.

  Query Match           55.6%;  Score 15;  DB 1;  Length 20;
  Best Local Similarity 89.5%;  Pred. No. 1.56e+01;
  Matches   17;  Conservative    0;  Mismatches   2;  Indels   0;  Gaps   0;

Db      1 TCAGATTCTGACGCTCAAA 19
          |||||  |||||||||||
Cp     25 TCAGACCCTGAGGCTCAAA 7


RESULT    7
ID   US-08-761-131-7 STANDARD; DNA; UNC; 20 BP.
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AC   xxxxxx
DT
DE   Sequence 7, Application US/08761131
CC   Sequence 7, Application US/08761131
CC   Patent No. 5804384
CC    GENERAL INFORMATION:
CC      APPLICANT:  M ller, Uwe R. et al.
CC      TITLE OF INVENTION:  DEVICES AND METHODS FOR DETECTING
CC      TITLE OF INVENTION:  MULTIPLE ANALYTES IN SAMPLES
CC      NUMBER OF SEQUENCES:  7
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Vysis, Inc.
CC        STREET:  3100 Woodcreek Drive
CC        CITY:  Downers Grove
CC        STATE:  Illinois
CC        COUNTRY:  U.S.A.
CC        ZIP:  60515
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Diskette
CC        COMPUTER:  IBM Compatible
CC        OPERATING SYSTEM:  DOS
CC        SOFTWARE:  FastSEQ Version 2.0
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/761,131
CC        FILING DATE:
CC        CLASSIFICATION:  435
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:
CC        FILING DATE:
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Galloway, No. 5804384val B.
CC        REGISTRATION NUMBER:  33,595
CC        REFERENCE/DOCKET NUMBER:  01886/064001
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  708-271-7417
CC        TELEFAX:  708-271-7048
CC        TELEX:  200154
CC    INFORMATION FOR SEQ ID NO:  7:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  20 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  single
CC        TOPOLOGY:  linear
CC      MOLECULE TYPE:  Genomic DNA
SQ   SEQUENCE 20 BP; 7 A; 4 C; 5 G; 4 T; 0 OTHER.

  Query Match           55.6%;  Score 15;  DB 3;  Length 20;
  Best Local Similarity 100.0%;  Pred. No. 1.56e+01;
  Matches   15;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Db      1 AGGCTCAAAGTCAGA 15
          ||||||||||||||
Cp     15 AGGCTCAAAGTCAGA 1


RESULT    8
ID   US-08-761-131-2 STANDARD; DNA; UNC; 40 BP.
AC   xxxxxx
DT
DE   Sequence 2, Application US/08761131
CC   Sequence 2, Application US/08761131
CC   Patent No. 5804384
CC    GENERAL INFORMATION:
CC      APPLICANT:  M ller, Uwe R. et al.
CC      TITLE OF INVENTION:  DEVICES AND METHODS FOR DETECTING
CC      TITLE OF INVENTION:  MULTIPLE ANALYTES IN SAMPLES
CC      NUMBER OF SEQUENCES:  7
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Vysis, Inc.
CC        STREET:  3100 Woodcreek Drive
CC        CITY:  Downers Grove
CC        STATE:  Illinois
CC        COUNTRY:  U.S.A.
CC        ZIP:  60515
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Diskette
CC        COMPUTER:  IBM Compatible
CC        OPERATING SYSTEM:  DOS
CC        SOFTWARE:  FastSEQ Version 2.0
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/761,131
CC        FILING DATE:
CC        CLASSIFICATION:  435
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:
CC        FILING DATE:
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Galloway, No. 5804384val B.
CC        REGISTRATION NUMBER:  33,595
CC        REFERENCE/DOCKET NUMBER:  01886/064001
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  708-271-7417
CC        TELEFAX:  708-271-7048
CC        TELEX:  200154
CC    INFORMATION FOR SEQ ID NO:  2:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  40 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  single
CC        TOPOLOGY:  linear
CC      MOLECULE TYPE:  Genomic DNA
SQ   SEQUENCE 40 BP; 10 A; 10 C; 8 G; 12 T; 0 OTHER.

  Query Match           55.6%;  Score 15;  DB 3;  Length 40;
  Best Local Similarity 60.0%;  Pred. No. 1.56e+01;
  Matches   9;  Conservative   6;  Mismatches   0;  Indels   0;  Gaps   0;

Db     26 TCTGACTTTGAGCCT 40
          :|:|||:::|||||:
Qy      1 UCUGACUUUGAGCCU 15


RESULT    9
ID   US-08-761-131-1 STANDARD; DNA; UNC; 40 BP.
AC   xxxxxx
DT
DE   Sequence 1, Application US/08761131
CC   Sequence 1, Application US/08761131
CC   Patent No. 5804384
CC    GENERAL INFORMATION:
CC      APPLICANT:  M ller, Uwe R. et al.
CC      TITLE OF INVENTION:  DEVICES AND METHODS FOR DETECTING
CC      TITLE OF INVENTION:  MULTIPLE ANALYTES IN SAMPLES
CC      NUMBER OF SEQUENCES:  7
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Vysis, Inc.
CC        STREET:  3100 Woodcreek Drive
CC        CITY:  Downers Grove
CC        STATE:  Illinois
CC        COUNTRY:  U.S.A.
CC        ZIP:  60515
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Diskette
CC        COMPUTER:  IBM Compatible
CC        OPERATING SYSTEM:  DOS
CC        SOFTWARE:  FastSEQ Version 2.0
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/761,131
CC        FILING DATE:
CC        CLASSIFICATION:  435
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:
CC        FILING DATE:
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Galloway, No. 5804384val B.
CC        REGISTRATION NUMBER:  33,595
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CC         REFERENCE/DOCKET NUMBER:  01886/064001
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  708-271-7417
CC         TELEFAX:  708-271-7048
CC         TELEX:  200154
CC     INFORMATION FOR SEQ ID NO:  1:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  40 base pairs
CC         TYPE:  nucleic acid
CC         STRANDEDNESS:  single
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  Genomic DNA
SQ   SEQUENCE 40 BP; 10 A; 13 C; 7 G; 10 T; 0 OTHER.

  Query Match           55.6%;  Score 15;  DB 3;  Length 40;
  Best Local Similarity  60.0%;  Pred. No. 1.56e+01;
  Matches     9;  Conservative     6;  Mismatches    0;  Indels    0;  Gaps    0;

Db      26 TCTGACTTTGAGCCT 40
           :|:|||:::|||||:
Qy       1 UCUGACUUUGAGCCU 15


RESULT   10
ID   PCT-US95-13041-13 STANDARD; DNA; UNC; 27 BP.
AC   xxxxxx
DT
DE   Sequence 13, Application PC/TUS9513041
CC   Sequence 13, Application PC/TUS9513041
CC    GENERAL INFORMATION:
CC      APPLICANT:  WHITE, Morris F.
CC      APPLICANT:  SUN, Xiao Jian
CC      APPLICANT:  PIERCE, Jacalyn H.
CC      TITLE OF INVENTION:  THE IRS FAMILY OF GENES
CC      NUMBER OF SEQUENCES:  63
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  LAHIVE & COCKFIELD
CC        STREET:  60 State Street, Suite 510
CC        CITY:  Boston
CC        STATE:  Massachusetts
CC        COUNTRY:  USA
CC        ZIP:  02109-1875
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  ASCII text
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  PCT/US95/13041
CC        FILING DATE:  Herewith
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  08/317,310
CC        FILING DATE:  03-OCT-1994
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Louis Myers
CC        REGISTRATION NUMBER:  35,965
CC        REFERENCE/DOCKET NUMBER:  JDP-022PC
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  (617)227-7400
CC        TELEFAX:  (617)227-5941
CC     INFORMATION FOR SEQ ID NO:  13:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  27 base pairs
CC         TYPE:  nucleic acid
CC         STRANDEDNESS:  single
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  cDNA
SQ   SEQUENCE 27 BP; 7 A; 10 C; 6 G; 3 T; 1 OTHER.

  Query Match           48.1%;  Score 13;  DB 4;  Length 27;
  Best Local Similarity  86.7%;  Pred. No. 1.55e+02;
  Matches    13;  Conservative     1;  Mismatches    1;  Indels    0;  Gaps    0;

Db      11 ACCCARACCCTGAGG 25
           || ||:|||||||||
Cp      27 ACTCAGACCCTGAGG 13


RESULT   11
ID   US-08-463-224-61 STANDARD; DNA; UNC; 33 BP.
AC   xxxxxx
DT
DE   Sequence 61, Application US/08463224
CC   Sequence 61, Application US/08463224
CC   Patent No. 5807824
CC    GENERAL INFORMATION:
CC      APPLICANT:  van Oostrum, Jan
CC      APPLICANT:  Boyar, William C.
CC      APPLICANT:  Galakatos, Nicholas G.
CC      APPLICANT:  Schmitz, Albert
CC      APPLICANT:  van Heeke, Gino
CC      TITLE OF INVENTION:  C5a Receptor Antagonists Having
CC      TITLE OF INVENTION:  Substantially No. 5807824Agonist Activity
CC      NUMBER OF SEQUENCES:  67
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Lerner, David, Littenberg, Krumholz & Mentlik
CC        STREET:  600 South Avenue West
CC        CITY:  Westfield
CC        STATE:  NJ
CC        COUNTRY:  USA
CC        ZIP:  07090
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, Version #1.25
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/463,224
CC        FILING DATE:
CC        CLASSIFICATION:  435
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Foley, Shawn P.
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  908-654-5000
CC        TELEFAX:  908-654-7866
CC        TELEX:  139-125
CC     INFORMATION FOR SEQ ID NO:  61:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  33 base pairs
CC         TYPE:  nucleic acid
CC         STRANDEDNESS:  single
CC         TOPOLOGY:  linear
SQ   SEQUENCE 33 BP; 11 A; 6 C; 9 G; 7 T; 0 OTHER.

  Query Match           48.1%;  Score 13;  DB 3;  Length 33;
  Best Local Similarity  88.2%;  Pred. No. 1.55e+02;
  Matches    15;  Conservative     0;  Mismatches    2;  Indels    0;  Gaps    0;

Db      12 CAGAGCATGAGGCTCAA 28
           |||| | ||||||||||
Cp      24 CAGACCCTGAGGCTCAA 8


RESULT   12
ID   US-08-645-641-25 STANDARD; DNA; UNC; 42 BP.
AC   xxxxxx
DT
DE   Sequence 25, Application US/08645641
CC   Sequence 25, Application US/08645641
CC   Patent No. 5719032
CC    GENERAL INFORMATION:
CC      APPLICANT:  Lonberg, Nils
CC      APPLICANT:  Kay, Robert M.
CC      TITLE OF INVENTION:  Transgenic No. 5719032-Human Animals for
CC      TITLE OF INVENTION:  Producing Heterologous Antibodies
CC      NUMBER OF SEQUENCES:  150
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CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  William M. Smith
CC        STREET:  Two Embarcadero Center, 8th Floor
CC        CITY:  San Francisco
CC        STATE:  California
CC        COUNTRY:  USA
CC        ZIP:  94111-3834
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, Version #1.25
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/645,641
CC        FILING DATE:  20-MAY-1996
CC        CLASSIFICATION:  800
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  US 07/904,068
CC        FILING DATE:  23-JUN-1992
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Smith, William M.
CC        REGISTRATION NUMBER:  30,223
CC        REFERENCE/DOCKET NUMBER:  14643-000913
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  415-326-2400
CC        TELEFAX:  415-326-2422
CC    INFORMATION FOR SEQ ID NO:  25:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  42 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  single
CC        TOPOLOGY:  linear
CC      MOLECULE TYPE:  DNA (primer)
SQ   SEQUENCE 42 BP; 10 A; 11 C; 15 G; 6 T; 0 OTHER.

  Query Match           48.1%;  Score 13;  DB 2;  Length 42;
  Best Local Similarity  68.4%;  Pred. No. 1.55e+02;
  Matches    13;  Conservative    3;  Mismatches   3;  Indels   0;  Gaps   0;

Db      3 CTGAAATGGAGCCTCAGGG 21
          |:||  : |||||:|||||
Qy      2 CUGACUUUGAGCCUCAGGG 20


RESULT   13
ID   US-08-053-131-25 STANDARD; DNA; UNC; 42 BP.
AC   xxxxxx
DT
DE   Sequence 25, Application US/08053131
CC   Sequence 25, Application US/08053131
CC   Patent No. 5661016
CC    GENERAL INFORMATION:
CC      APPLICANT:  Lonberg, Nils
CC      APPLICANT:  Kay, Robert M.
CC      TITLE OF INVENTION:  Transgenic No. 5661016-Human Animals for
CC      TITLE OF INVENTION:  Producing Heterologous Antibodies
CC      NUMBER OF SEQUENCES:  197
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Townsend and Townsend Khourie and Crew
CC        STREET:  One Market Plaza, Steuart Tower, Suite 200
CC        CITY:  San Francisco
CC        STATE:  California
CC        COUNTRY:  USA
CC        ZIP:  94105
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, Version #1.25
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/053,131
CC        FILING DATE:  26-APR-1993
CC        CLASSIFICATION:  800
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  US 07/990,860
CC        FILING DATE:  16-DEC-1992
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  US 07/810,279
CC        FILING DATE:  17-DEC-1991
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  US 07/853,408
CC        FILING DATE:  18-MAR-1992
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Smith, William M.
CC        REGISTRATION NUMBER:  30,223
CC        REFERENCE/DOCKET NUMBER:  14643-9-3
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  415-326-2400
CC        TELEFAX:  415-326-2422
CC    INFORMATION FOR SEQ ID NO:  25:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  42 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  single
CC        TOPOLOGY:  linear
CC      MOLECULE TYPE:  DNA (primer)
SQ   SEQUENCE 42 BP; 10 A; 11 C; 15 G; 6 T; 0 OTHER.

  Query Match           48.1%;  Score 13;  DB 2;  Length 42;
  Best Local Similarity  68.4%;  Pred. No. 1.55e+02;
  Matches    13;  Conservative    3;  Mismatches   3;  Indels   0;  Gaps   0;

Db      3 CTGAAATGGAGCCTCAGGG 21
          |:||  : |||||:|||||
Qy      2 CUGACUUUGAGCCUCAGGG 20


RESULT   14
ID   US-08-096-762-25 STANDARD; DNA; UNC; 42 BP.
AC   xxxxxx
DT
DE   Sequence 25, Application US/08096762
CC   Sequence 25, Application US/08096762
CC   Patent No. 5814318
CC    GENERAL INFORMATION:
CC      APPLICANT:  Lonberg, Nils
CC      APPLICANT:  Kay, Robert M.
CC      TITLE OF INVENTION:  Transgenic No. 5814318-Human Animals for
CC      TITLE OF INVENTION:  Producing Heterologous Antibodies
CC      NUMBER OF SEQUENCES:  210
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Townsend and Townsend Khourie and Crew
CC        STREET:  One Market Plaza, Steuart Tower, Suite 200
CC        CITY:  San Francisco
CC        STATE:  California
CC        COUNTRY:  USA
CC        ZIP:  94105
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, Version #1.25
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/096,762
CC        FILING DATE:  22-JUL-1993
CC        CLASSIFICATION:  800
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  US 08/053,131
CC        FILING DATE:  26-APR-1993
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  US 07/990,860
CC        FILING DATE:  16-DEC-1992
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  US 07/904,068
CC        FILING DATE:  23-JUN-1992
CC      PRIOR APPLICATION DATA:
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CC       APPLICATION NUMBER:  US 07/853,408
CC       FILING DATE:  18-MAR-1992
CC     PRIOR APPLICATION DATA:
CC       APPLICATION NUMBER:  US 07/810,279
CC       FILING DATE:  17-DEC-1991
CC     ATTORNEY/AGENT INFORMATION:
CC       NAME:  Smith, William M.
CC       REGISTRATION NUMBER:  30,223
CC       REFERENCE/DOCKET NUMBER:  14643-9-4
CC     TELECOMMUNICATION INFORMATION:
CC       TELEPHONE:  415-326-2400
CC       TELEFAX:  415-326-2422
CC   INFORMATION FOR SEQ ID NO:  25:
CC     SEQUENCE CHARACTERISTICS:
CC       LENGTH:  42 base pairs
CC       TYPE:  nucleic acid
CC       STRANDEDNESS:  single
CC       TOPOLOGY:  linear
CC     MOLECULE TYPE:  DNA (primer)
SQ   SEQUENCE 42 BP; 10 A; 11 C; 15 G; 6 T; 0 OTHER.

  Query Match           48.1%;  Score 13;  DB 3;  Length 42;
  Best Local Similarity  68.4%;  Pred. No. 1.55e+02;
  Matches   13;  Conservative    3;  Mismatches   3;  Indels   0;  Gaps   0;

Db       3 CTGAAATGGAGCCTCAGGG 21
           |:||  : |||||:|||||
Qy       2 CUGACUUUGAGCCUCAGGG 20


RESULT   15
ID   PCT-US92-06185-17 STANDARD; DNA; UNC; 42 BP.
AC   xxxxxx
DT
DE   Sequence 17, Application PC/TUS9206185
CC   Sequence 17, Application PC/TUS9206185
CC    GENERAL INFORMATION:
CC      APPLICANT:  Lonberg, Nils
CC      APPLICANT:  Kay, Robert M.
CC      TITLE OF INVENTION:  Transgenic Non-Human Animals Capable of
CC      TITLE OF INVENTION:  Producing Heterologous Antibodies
CC      NUMBER OF SEQUENCES:  75
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  William M. Smith
CC        STREET:  One Market Plaza, Steuart Tower, Suite 2000
CC        CITY:  San Francisco
CC        STATE:  California
CC        COUNTRY:  USA
CC        ZIP:  94105
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, Version #1.25
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  PCT/US92/06185
CC        FILING DATE:  19910828
CC        CLASSIFICATION:
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Smith, William M.
CC        REGISTRATION NUMBER:  87654
CC        REFERENCE/DOCKET NUMBER:  14643-5
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  415-543-9600
CC        TELEFAX:  415-543-5043
CC    INFORMATION FOR SEQ ID NO:  17:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  42 base pairs
CC        TYPE:  NUCLEIC ACID
CC        STRANDEDNESS:  single
CC        TOPOLOGY:  linear
CC      MOLECULE TYPE:  DNA (genomic)
SQ   SEQUENCE 42 BP; 10 A; 11 C; 15 G; 6 T; 0 OTHER.

  Query Match           48.1%;  Score 13;  DB 4;  Length 42;
  Best Local Similarity  68.4%;  Pred. No. 1.55e+02;
  Matches   13;  Conservative    3;  Mismatches   3;  Indels   0;  Gaps   0;

Db       3 CTGAAATGGAGCCTCAGGG 21
           |:||  : |||||:|||||
Qy       2 CUGACUUUGAGCCUCAGGG 20


RESULT   16
ID   US-07-834-539A-17 STANDARD; DNA; UNC; 42 BP.
AC   xxxxxx
DT
DE   Sequence 17, Application US/07834539A
CC   Sequence 17, Application US/07834539A
CC    GENERAL INFORMATION:
CC      APPLICANT:  Lonberg, Nils
CC      APPLICANT:  Kay, Robert M.
CC      TITLE OF INVENTION:  Transgenic Non-Human Animals Capable of
CC      TITLE OF INVENTION:  Producing Heterologous Antibodies
CC      NUMBER OF SEQUENCES:  77
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  William M. Smith
CC        STREET:  One Market Plaza, Steuart Tower, Suite 2000
CC        CITY:  San Francisco
CC        STATE:  California
CC        COUNTRY:  USA
CC        ZIP:  94105
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, Version #1.25
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/07/834,539A
CC        FILING DATE:  1992-02-05
CC        CLASSIFICATION:
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Smith, William M.
CC        REGISTRATION NUMBER:  30,223
CC        REFERENCE/DOCKET NUMBER:  14643-5
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  415-543-9600
CC        TELEFAX:  415-543-5043
CC    INFORMATION FOR SEQ ID NO:  17:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  42 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  single
CC        TOPOLOGY:  linear
CC      MOLECULE TYPE:  DNA (genomic)
SQ   SEQUENCE 42 BP; 10 A; 11 C; 15 G; 6 T; 0 OTHER.

  Query Match           48.1%;  Score 13;  DB 1;  Length 42;
  Best Local Similarity  68.4%;  Pred. No. 1.55e+02;
  Matches   13;  Conservative    3;  Mismatches   3;  Indels   0;  Gaps   0;

Db       3 CTGAAATGGAGCCTCAGGG 21
           |:||  : |||||:|||||
Qy       2 CUGACUUUGAGCCUCAGGG 20


RESULT   17
ID   PCT-US92-10983-25 STANDARD; DNA; UNC; 42 BP.
AC   xxxxxx
DT
DE   Sequence 25, Application PC/TUS9210983
CC   Sequence 25, Application PC/TUS9210983
CC    GENERAL INFORMATION:
CC      APPLICANT:  Lonberg, Nils
CC      APPLICANT:  Kay, Robert M.
CC      TITLE OF INVENTION:  Transgenic Non-Human Animals for
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CC      TITLE OF INVENTION:  Producing Heterologous Antibodies
CC      NUMBER OF SEQUENCES:  152
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  William M. Smith
CC        STREET:  One Market Plaza, Steuart Tower, Suite 2000
CC        CITY:  San Francisco
CC        STATE:  California
CC        COUNTRY:  USA
CC        ZIP:  94105
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, Version #1.25
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  PCT/US92/10983
CC        FILING DATE:  19921217
CC        CLASSIFICATION:
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Smith, William M.
CC        REGISTRATION NUMBER:  30,223
CC        REFERENCE/DOCKET NUMBER:  14643-9-2
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  415-326-2400
CC        TELEFAX:  415-326-2422
CC    INFORMATION FOR SEQ ID NO:  25:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  42 base pairs
CC        TYPE:  NUCLEIC ACID
CC        STRANDEDNESS:  single
CC        TOPOLOGY:  linear
CC      MOLECULE TYPE:  DNA (primer)
SQ   SEQUENCE 42 BP; 10 A; 11 C; 15 G; 6 T; 0 OTHER.

  Query Match           48.1%;  Score 13;  DB 4;  Length 42;
  Best Local Similarity  68.4%;  Pred. No. 1.55e+02;
  Matches    13;  Conservative    3;  Mismatches   3;  Indels   0;  Gaps   0;

Db       3 CTGAAATGGAGCCTCAGGG 21
           |:||  : |||||:|||||
Qy       2 CUGACUUUGAGCCUCAGGG 20


RESULT   18
ID   US-07-853-408B-25 STANDARD; DNA; UNC; 42 BP.
AC   xxxxxx
DT
DE   Sequence 25, Application US/07853408B
CC   Sequence 25, Application US/07853408B
CC   Patent No. 5789650
CC    GENERAL INFORMATION:
CC      APPLICANT:  Lonberg, Nils
CC      APPLICANT:  Kay, Robert M.
CC      TITLE OF INVENTION:  Transgenic No. 5789650-Human Animals for
CC      TITLE OF INVENTION:  Producing Heterologous Antibodies
CC      NUMBER OF SEQUENCES:  150
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  William M. Smith
CC        STREET:  One Market Plaza, Steuart Tower, Suite 2000
CC        CITY:  San Francisco
CC        STATE:  California
CC        COUNTRY:  USA
CC        ZIP:  94105
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, Version #1.25
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/07/853,408B
CC        FILING DATE:  19920318
CC        CLASSIFICATION:  800
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Smith, William M.
CC        REGISTRATION NUMBER:  30,223
CC        REFERENCE/DOCKET NUMBER:  14643-9
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  415-326-2400
CC        TELEFAX:  415-326-2422
CC    INFORMATION FOR SEQ ID NO:  25:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  42 base pairs
CC        TYPE:  NUCLEIC ACID
CC        STRANDEDNESS:  single
CC        TOPOLOGY:  linear
CC      MOLECULE TYPE:  DNA (primer)
SQ   SEQUENCE 42 BP; 10 A; 11 C; 15 G; 6 T; 0 OTHER.

  Query Match           48.1%;  Score 13;  DB 3;  Length 42;
  Best Local Similarity  68.4%;  Pred. No. 1.55e+02;
  Matches    13;  Conservative    3;  Mismatches   3;  Indels   0;  Gaps   0;

Db       3 CTGAAATGGAGCCTCAGGG 21
           |:||  : |||||:|||||
Qy       2 CUGACUUUGAGCCUCAGGG 20


RESULT   19
ID   US-08-399-696-53 STANDARD; DNA; UNC; 45 BP.
AC   xxxxxx
DT
DE   Sequence 53, Application US/08399696
CC   Sequence 53, Application US/08399696
CC   Patent No. 5756669
CC    GENERAL INFORMATION:
CC      APPLICANT:
CC      TITLE OF INVENTION:  p53-BINDING POLYPEPTIDES AND
CC      TITLE OF INVENTION:  POLYNUCLEOTIDES ENCODING SAME
CC      NUMBER OF SEQUENCES:  126
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, Version #1.25
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/399,696
CC        FILING DATE:  02-MAR-1995
CC        CLASSIFICATION:  435
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  US 08/156,671
CC        FILING DATE:  22-NOV-1993
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Smith, William M
CC        REGISTRATION NUMBER:  30,223
CC        REFERENCE/DOCKET NUMBER:  15522-000710
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  (415) 326-2400
CC        TELEFAX:  (415) 326-2422
CC    INFORMATION FOR SEQ ID NO:  53:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  45 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  single
CC        TOPOLOGY:  linear
CC      MOLECULE TYPE:  DNA
SQ   SEQUENCE 45 BP; 7 A; 14 C; 12 G; 12 T; 0 OTHER.

  Query Match           48.1%;  Score 13;  DB 3;  Length 45;
  Best Local Similarity  58.8%;  Pred. No. 1.55e+02;
  Matches    10;  Conservative    5;  Mismatches   2;  Indels   0;  Gaps   0;

Db      21 CTGCTTTTGAGCCTCAG 37
           |:|  :::|||||:|||
Qy       2 CUGACUUUGAGCCUCAG 18
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RESULT   20
ID   PCT-US96-08014-269 STANDARD; DNA; UNC; 26 BP.
AC   xxxxxx
DT
DE   Sequence 269, Application PC/TUS9608014
CC   Sequence 269, Application PC/TUS9608014
CC    GENERAL INFORMATION:
CC      APPLICANT:  LARRY GOLD; NEBOJSA JANJIC; STEVEN RINGQUIST;    NIKOS
CC      APPLICANT:  PAGRATIS;PENELOPE J. TOOTHMAN
CC      TITLE OF INVENTION:  HIGH AFFINITY OLIGONUCLEOTIDE
CC      TITLE OF INVENTION:  LIGANDS TO TRANSFORMING GROWTH
CC      TITLE OF INVENTION:  FACTOR   (TGF ), PLATELET-DERIVED
CC      TITLE OF INVENTION:  GROWTH FACTOR (PDGF) AND HUMAN
CC      TITLE OF INVENTION:  KEROTINOCYTE GROWTH FACTOR (hKGF)
CC      NUMBER OF SEQUENCES:  304
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Swanson & Bratschun, L.L.C.
CC        STREET:  8400 E. Prentice Avenue, Suite 200
CC        CITY:  Englewood
CC        STATE:  Colorado
CC        COUNTRY:  USA
CC        ZIP:  80111
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Diskette, 3.5 inch, 1.44 Mb storage
CC        COMPUTER:  IBM compatible
CC        OPERATING SYSTEM:  MS-DOS
CC        SOFTWARE:  WordPerfect 6.1
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  PCT/US96/08014
CC        FILING DATE:
CC        CLASSIFICATION:
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  08/458,423
CC        FILING DATE:  02-JUNE-1995
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  08/458,424
CC        FILING DATE:  02-JUNE-1995
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  08/465,594
CC        FILING DATE:  05-JUNE-1995
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  08/465,591
CC        FILING DATE:  05-JUNE-1995
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  08/479,725
CC        FILING DATE:  07-JUNE-1995
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  08/479,783
CC        FILING DATE:  07-JUNE-1995
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  08/618,693
CC        FILING DATE:  20-MARCH-1996
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Barry J. Swanson
CC        REGISTRATION NUMBER:  33,215
CC        REFERENCE/DOCKET NUMBER:
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  (303) 793-3333
CC        TELEFAX:  (303) 793-3433
CC    INFORMATION FOR SEQ ID NO:  269:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  26 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  single
CC        TOPOLOGY:  linear
CC      MOLECULE TYPE:  RNA
CC      FEATURE:
CC        OTHER INFORMATION:  All pyrimidines are 2'-fluoro (2'-F) modified
SQ   SEQUENCE 26 BP; 1 A; 0 C; 3 G; 0 T; 22 OTHER.

  Query Match           44.4%;  Score 12;  DB 4;  Length 26;
  Best Local Similarity   5.0%;  Pred. No. 4.61e+02;
  Matches     1;  Conservative   15;  Mismatches   4;  Indels   0;  Gaps   0;

Db       7 RAYYRSBRSYYYYBSYBSY 26
           :|::  :::::: :: :::
Qy       4 GACUUUGAGCCUCAGGGUCU 23


RESULT   21
ID   US-08-428-733A-39 STANDARD; DNA; UNC; 37 BP.
AC   xxxxxx
DT
DE   Sequence 39, Application US/08428733A
CC   Sequence 39, Application US/08428733A
CC   Patent No. 5763284
CC    GENERAL INFORMATION:
CC      APPLICANT:  Tal, Rony
CC      APPLICANT:  Wong, Hing C.
CC      APPLICANT:  Casipit, Clayton
CC      APPLICANT:  Chavaillaz, Pierre-Andre
CC      APPLICANT:  Wittman, Vaughan
CC      TITLE OF INVENTION:  Methods for Peptide Synthesis and
CC      TITLE OF INVENTION:  Purification
CC      NUMBER OF SEQUENCES:  57
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  DADE INTERNATIONAL, INC.
CC        STREET:  1717 Deerfield Road
CC        CITY:  Deerfield
CC        STATE:  Illinois
CC        COUNTRY:  US
CC        ZIP:  60015
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, Version #1.25
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/428,733A
CC        FILING DATE:  04-APR-1995
CC        CLASSIFICATION:  435
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  US 08/235,178
CC        FILING DATE:  29-APR-1994
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Pearson, Louise S.
CC        REGISTRATION NUMBER:  32,369
CC        REFERENCE/DOCKET NUMBER:  DA-4623 CIP
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  (708) 267-5300
CC        TELEFAX:  (708) 267-5376
CC    INFORMATION FOR SEQ ID NO:  39:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  37 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  unknown
CC        TOPOLOGY:  unknown
SQ   SEQUENCE 37 BP; 8 A; 14 C; 8 G; 7 T; 0 OTHER.

  Query Match           44.4%;  Score 12;  DB 3;  Length 37;
  Best Local Similarity  58.3%;  Pred. No. 4.61e+02;
  Matches    14;  Conservative    4;  Mismatches   6;  Indels   0;  Gaps   0;

Db      12 GACCTTCAGCTGCACGGTCAGAGT 35
           ||| :: ||| . || ||:| |||:
Qy       4 GACUUUGAGCCUCAGGGUCUGAGU 27


RESULT   22
ID   US-08-428-733A-7 STANDARD; DNA; UNC; 37 BP.
AC   xxxxxx
DT
DE   Sequence 7, Application US/08428733A
CC   Sequence 7, Application US/08428733A
CC   Patent No. 5763284
CC    GENERAL INFORMATION:
```

```
CC       APPLICANT:  Tal, Rony
CC       APPLICANT:  Wong, Hing C.
CC       APPLICANT:  Casipit, Clayton
CC       APPLICANT:  Chavaillaz, Pierre-Andre
CC       APPLICANT:  Wittman, Vaughan
CC       TITLE OF INVENTION:  Methods for Peptide Synthesis and
CC       TITLE OF INVENTION:  Purification
CC       NUMBER OF SEQUENCES:  57
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  DADE INTERNATIONAL, INC.
CC         STREET:  1717 Deerfield Road
CC         CITY:  Deerfield
CC         STATE:  Illinois
CC         COUNTRY:  US
CC         ZIP:  60015
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, Version #1.25
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/428,733A
CC         FILING DATE:  04-APR-1995
CC         CLASSIFICATION:  435
CC       PRIOR APPLICATION DATA:
CC         APPLICATION NUMBER:  US 08/235,178
CC         FILING DATE:  29-APR-1994
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Pearson, Louise S.
CC         REGISTRATION NUMBER:  32,369
CC         REFERENCE/DOCKET NUMBER:  DA-4623 CIP
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  (708) 267-5300
CC         TELEFAX:  (708) 267-5376
CC     INFORMATION FOR SEQ ID NO:  7:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  37 base pairs
CC         TYPE:  nucleic acid
CC         STRANDEDNESS:  unknown
CC         TOPOLOGY:  unknown
SQ   SEQUENCE 37 BP; 7 A; 9 C; 13 G; 8 T; 0 OTHER.

  Query Match           44.4%;  Score 12;  DB 3;  Length 37;
  Best Local Similarity  75.0%;  Pred. No. 4.61e+02;
  Matches    18;  Conservative    0;  Mismatches   6;  Indels   0;  Gaps   0;

Db       2 ACTCTGACCGTGCAGCTGAAGGTC 25
          |||| |||| ||  ||| || |||
Cp      27 ACTCAGACCCTGAGGCTCAAAGTC 4


RESULT   23
ID   US-08-428-733A-38 STANDARD; DNA; UNC; 37 BP.
AC   xxxxxx
DT
DE   Sequence 38, Application US/08428733A
CC   Sequence 38, Application US/08428733A
CC   Patent No. 5763284
CC    GENERAL INFORMATION:
CC      APPLICANT:  Tal, Rony
CC      APPLICANT:  Wong, Hing C.
CC      APPLICANT:  Casipit, Clayton
CC      APPLICANT:  Chavaillaz, Pierre-Andre
CC      APPLICANT:  Wittman, Vaughan
CC      TITLE OF INVENTION:  Methods for Peptide Synthesis and
CC      TITLE OF INVENTION:  Purification
CC      NUMBER OF SEQUENCES:  57
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  DADE INTERNATIONAL, INC.
CC        STREET:  1717 Deerfield Road
CC        CITY:  Deerfield
CC        STATE:  Illinois
CC        COUNTRY:  US
CC        ZIP:  60015
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, Version #1.25
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/428,733A
CC        FILING DATE:  04-APR-1995
CC        CLASSIFICATION:  435
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  US 08/235,178
CC        FILING DATE:  29-APR-1994
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Pearson, Louise S.
CC        REGISTRATION NUMBER:  32,369
CC        REFERENCE/DOCKET NUMBER:  DA-4623 CIP
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  (708) 267-5300
CC        TELEFAX:  (708) 267-5376
CC    INFORMATION FOR SEQ ID NO:  38:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  37 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  unknown
CC        TOPOLOGY:  unknown
SQ   SEQUENCE 37 BP; 7 A; 8 C; 14 G; 8 T; 0 OTHER.

  Query Match           44.4%;  Score 12;  DB 3;  Length 37;
  Best Local Similarity  75.0%;  Pred. No. 4.61e+02;
  Matches    18;  Conservative    0;  Mismatches   6;  Indels   0;  Gaps   0;

Db       7 ACTCTGACCGTGCAGCTGAAGGTC 30
          |||| |||| ||  ||| || |||
Cp      27 ACTCAGACCCTGAGGCTCAAAGTC 4


RESULT   24
ID   PCT-US95-07201-19 STANDARD; DNA; UNC; 24 BP.
AC   xxxxxx
DT
DE   Sequence 19, Application PC/TUS9507201
CC   Sequence 19, Application PC/TUS9507201
CC    GENERAL INFORMATION:
CC      APPLICANT:  Chader, Gerald J.; Becerra, Sofia
CC      APPLICANT:  Patricia; Schwartz, Joan P.;
CC      APPLICANT:  Taniwaki, Takayuki
CC      TITLE OF INVENTION:  PIGMENT EPITHELIUM
CC      TITLE OF INVENTION:  DERIVED FACTOR; CHARACTERIZATION GENOMIC
CC      TITLE OF INVENTION:  ORGANIZATION AND SEQUENCE OF THE PEDF GENE
CC      NUMBER OF SEQUENCES:  43
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Morgan & Finnegan, L.L.P.
CC        STREET:  345 Park Avenue
CC        CITY:  New York
CC        STATE:  New York
CC        COUNTRY:  USA
CC        ZIP:  10154
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy Disk
CC        COMPUTER:  IBM PC Compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  WORDPERFECT 5.1
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  PCT/US95/07201
CC        FILING DATE:  06-JUN-1995
CC        CLASSIFICATION:
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  08/367,841
CC        FILING DATE:  30-DEC-1994
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  08/257,963
CC        FILING DATE:  07-JUN-1994
```

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CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  07/952,796
CC        FILING DATE:  24-SEP-1992
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  DOROTHY R. AUTH
CC        REGISTRATION NUMBER:  36434
CC        REFERENCE/DOCKET NUMBER:  20264126PCT
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  (212) 758-4800
CC        TELEFAX:  (212) 751-6849
CC    INFORMATION FOR SEQ ID NO:  19:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  24 Base Pairs
CC        TYPE:  Nucleic Acid
CC        STRANDEDNESS:  Uknown
CC        TOPOLOGY:  Unknown
CC      MOLECULE TYPE:  Oligonucleotide
CC      FEATURE:
CC        NAME/KEY:  2238
CC        LOCATION:
CC        IDENTIFICATION METHOD:
CC        OTHER INFORMATION:  primer in a polymerase
CC        OTHER INFORMATION:  chain reaction
SQ   SEQUENCE 24 BP; 5 A; 5 C; 7 G; 7 T; 0 OTHER.

  Query Match           40.7%;  Score 11;  DB 4;  Length 24;
  Best Local Similarity  86.7%;  Pred. No. 1.31e+03;
  Matches   13;  Conservative    0;  Mismatches   2;  Indels   0;  Gaps   0;

Db      7 TCGGACCCTAAGGCT 21
          || |||||| |||||
Cp     25 TCAGACCCTGAGGCT 11


RESULT   25
ID   US-07-999-280A-20 STANDARD; DNA; UNC; 25 BP.
AC   xxxxxx
DT
DE   Sequence 20, Application US/07999280A
CC   Sequence 20, Application US/07999280A
CC   Patent No. 5573930
CC    GENERAL INFORMATION:
CC      APPLICANT:  LADNER, MARTHA B.
CC      APPLICANT:  NOBLE, JANELLE A.
CC      APPLICANT:  MARTIN, GEORGE A.
CC      APPLICANT:  KAWASAKI, ERNEST S.
CC      APPLICANT:  COYNE, MAZIE YEE
CC      APPLICANT:  HALENBECK, ROBERT F.
CC      APPLICANT:  KOTHS, KIRSTON E.
CC      TITLE OF INVENTION:  NEW FORMS OF COLONY STIMULATING FACTOR-1
CC      NUMBER OF SEQUENCES:  24
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  CHIRON CORPORATION
CC        STREET:  Intellectual Property - R440, P.O. Box 8097
CC        CITY:  Emveryville
CC        STATE:  California
CC        COUNTRY:  U.S.A.
CC        ZIP:  94662-8097
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, Version #1.25
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/07/999,280A
CC        FILING DATE:  28-DEC-1992
CC        CLASSIFICATION:  435
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  McGarrigle Jr., Philip L.
CC        REGISTRATION NUMBER:  31,395
CC        REFERENCE/DOCKET NUMBER:  0681.007
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  (510) 601-2718
CC        TELEFAX:  (510) 655-3542
CC        TELEX:  n/a
CC    INFORMATION FOR SEQ ID NO:  20:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  25 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  single
CC        TOPOLOGY:  linear
CC      MOLECULE TYPE:  DNA (genomic)
SQ   SEQUENCE 25 BP; 5 A; 6 C; 8 G; 6 T; 0 OTHER.

  Query Match           40.7%;  Score 11;  DB 1;  Length 25;
  Best Local Similarity  92.3%;  Pred. No. 1.31e+03;
  Matches   12;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db     13 TCAGACTCTGAGG 25
          |||||| |||||||
Cp     25 TCAGACCCTGAGG 13


RESULT   26
ID   US-08-758-306-426 STANDARD; DNA; UNC; 27 BP.
AC   xxxxxx
DT
DE   Sequence 426, Application US/08758306
CC   Sequence 426, Application US/08758306
CC   Patent No. 5807743
CC    GENERAL INFORMATION:
CC      APPLICANT:  Stinchcomb, Dan T.
CC      APPLICANT:  McSwiggen, James A.
CC      TITLE OF INVENTION:  METHOD AND REAGENT FOR THE
CC      TITLE OF INVENTION:  TREATMENT OF DISEASES
CC      TITLE OF INVENTION:  ASSOCIATED WITH
CC      TITLE OF INVENTION:  INTERLEUKIN-2 RECEPTOR
CC      TITLE OF INVENTION:  GAMMA-CHAIN EXPRESSION
CC      NUMBER OF SEQUENCES:  1379
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Lyon & Lyon
CC        STREET:  633 West Fifth Street
CC        STREET:  Suite 4700
CC        CITY:  Los Angeles
CC        STATE:  California
CC        COUNTRY:  U.S.A.
CC        ZIP:  90071-2066
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
CC        MEDIUM TYPE:  storage
CC        COMPUTER:  IBM Compatible
CC        OPERATING SYSTEM:  IBM P.C. DOS 5.0
CC        SOFTWARE:  FastSeq Version 1.5
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/758,306
CC        FILING DATE:  December 3, 1996
CC        CLASSIFICATION:  514
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:
CC        FILING DATE:
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Warburg, Richard J.
CC        REGISTRATION NUMBER:  32,327
CC        REFERENCE/DOCKET NUMBER:  212/132
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  (213) 489-1600
CC        TELEFAX:  (213) 955-0440
CC        TELEX:  67-3510
CC    INFORMATION FOR SEQ ID NO:  426:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  27 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  single
CC        TOPOLOGY:  linear
CC      FEATURE:
CC        OTHER INFORMATION:  The letter "N" stands for the stem II
```

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CC       OTHER INFORMATION:  region of a HH ribozyme.
SQ   SEQUENCE 27 BP; 10 A; 4 C; 9 G; 0 T; 4 OTHER.

  Query Match           40.7%;  Score 11;  DB 3;  Length 27;
  Best Local Similarity  66.7%;  Pred. No. 1.31e+03;
  Matches   16;  Conservative    1;  Mismatches   7;  Indels   0;  Gaps   0;

Db       3 CAGACUCUGAUGANGAAAGGGAGA 26
           ||||| |:|| |   ||||  |||
Cp      24 CAGACCCTGAGGCTCAAAGTCAGA 1


RESULT   27
ID   PCT-US95-06613-62 STANDARD; DNA; UNC; 29 BP.
AC   XXXXXX
DT
DE   Sequence 62, Application PC/TUS9506613
CC   Sequence 62, Application PC/TUS9506613
CC    GENERAL INFORMATION:
CC      APPLICANT:  STRACKE, MARY; LIOTTA, LANCE;
CC      APPLICANT:  SCHIFFMANN, ELLIOTT; KRUTZSCH,
CC      APPLICANT:  HENRY; MURATA, JUN
CC      TITLE OF INVENTION:  MOTILITY STIMULATING
CC      TITLE OF INVENTION:  PROTEIN USEFUL IN CANCER DIAGNOSIS AND
CC      TITLE OF INVENTION:  THERAPY
CC      NUMBER OF SEQUENCES:  69
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  MORGAN & FINNEGAN
CC        STREET:  345 PARK AVENUE
CC        CITY:  NEW YORK
CC        STATE:  NEW YORK
CC        COUNTRY:  U.S.A.
CC        ZIP:  10154
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy Disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  WordPerfect 5.1
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  PCT/US95/06613
CC        FILING DATE:  24-MAY-1995
CC        CLASSIFICATION:
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  08/346,455
CC        FILING DATE:  28-NOV-1994
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  08/249,182
CC        FILING DATE:  25-MAY-1994
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  07/822,043
CC        FILING DATE:  17-JAN-1992
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  DOROTHY R. AUTH
CC        REGISTRATION NUMBER:  36,434
CC        REFERENCE/DOCKET NUMBER:  2026-4149US2
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  (212) 758-4800
CC        TELEFAX:  (212) 751-6849
CC    INFORMATION FOR SEQ ID NO:  62:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  29
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  single
CC        TOPOLOGY:  linear
CC      MOLECULE TYPE:  cDNA
CC      HYPOTHETICAL:  No
CC      ANTI-SENSE:  No
CC      FEATURE:
CC        NAME/KEY:
CC        LOCATION:
CC        IDENTIFICATION METHOD:
CC        OTHER INFORMATION:  Nested primer deduced
CC        OTHER INFORMATION:  from ATX-103, wherein N is inosine

SQ   SEQUENCE 29 BP; 3 A; 6 C; 6 G; 4 T; 10 OTHER.

  Query Match           40.7%;  Score 11;  DB 4;  Length 29;
  Best Local Similarity  35.7%;  Pred. No. 1.31e+03;
  Matches    5;  Conservative    7;  Mismatches   2;  Indels   0;  Gaps   0;

Db       3 YTTYGARYTNCARG 16
           ::::||::  ||:|
Qy       6 CUUUGAGCCUCAGG 19


RESULT   28
ID   US-08-476-008-29 STANDARD; DNA; UNC; 31 BP.
AC   XXXXXX
DT
DE   Sequence 29, Application US/08476008
CC   Sequence 29, Application US/08476008
CC   Patent No. 5627061
CC    GENERAL INFORMATION:
CC      APPLICANT:  Barry, Gerard F.
CC      APPLICANT:  Kishore, Ganesh M.
CC      APPLICANT:  Padgette, Stephen R.
CC      APPLICANT:  Stallings, William C.
CC      TITLE OF INVENTION:  Glyphosate Tolerant
CC      TITLE OF INVENTION:  5-Enolpyruvylshikimate-3-Phosphate Synthases
CC      NUMBER OF SEQUENCES:  69
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Dennis R. Hoerner, Jr., Monsanto Co. BB4F
CC        STREET:  700 Chesterfield Village Parkway
CC        CITY:  St. Louis
CC        STATE:  Missouri
CC        COUNTRY:  USA
CC        ZIP:  63198
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, Version #1.25
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/476,008
CC        FILING DATE:  07-JUN-1995
CC        CLASSIFICATION:  435
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  US 08/306,063
CC        FILING DATE:  13-SEP-1994
CC        APPLICATION NUMBER:  US 07/749,611
CC        FILING DATE:  28-AUG-1991
CC        CLASSIFICATION:  435
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  US 07/576,537
CC        FILING DATE:  31-AUG-1990
CC        CLASSIFICATION:  435
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Hoerner Jr., Dennis R.
CC        REGISTRATION NUMBER:  30,914
CC        REFERENCE/DOCKET NUMBER:  38-21(10660)A
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  (314)537-6099
CC        TELEFAX:  (314)537-6047
CC    INFORMATION FOR SEQ ID NO:  29:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  31 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  single
CC        TOPOLOGY:  linear
CC      MOLECULE TYPE:  Other nucleic acid
CC        DESCRIPTION:  Synthetic DNA
SQ   SEQUENCE 31 BP; 2 A; 11 C; 12 G; 6 T; 0 OTHER.

  Query Match           40.7%;  Score 11;  DB 1;  Length 31;
  Best Local Similarity  60.0%;  Pred. No. 1.31e+03;
  Matches    9;  Conservative    4;  Mismatches   2;  Indels   0;  Gaps   0;
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Db      12 CTGACTATGGGCCTC 26
           |:|||: :| |||:|
Qy       2 CUGACUUUGAGCCUC 16


RESULT   29
ID   US-08-483-389-7 STANDARD; DNA; UNC; 31 BP.
AC   xxxxxx
DT
DE   Sequence 7, Application US/08483389
CC   Sequence 7, Application US/08483389
CC   Patent No. 5811517
CC    GENERAL INFORMATION:
CC      APPLICANT:  Gallatin, W. Michael
CC      APPLICANT:  Vazeux, Rosemay
CC      TITLE OF INVENTION:  ICAM-RELATED PROTEIN
CC      NUMBER OF SEQUENCES:  118
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
CC        STREET:  233 South Wacker Drive/6300 Sears Tower
CC        CITY:  Chicago
CC        STATE:  Illinois
CC        COUNTRY:  United States of America
CC        ZIP:  60606
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, Version #1.30
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/483,389
CC        FILING DATE:  07-JUN-1995
CC        CLASSIFICATION:  530
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  US 08/102,852
CC        FILING DATE:  05-AUG-1993
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  US 08/009,266
CC        FILING DATE:  22-JAN-1993
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  US 07/894,061
CC        FILING DATE:  05-JUN-1992
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  US 07/889,724
CC        FILING DATE:  26-MAY-1992
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  US 07/827,689
CC        FILING DATE:  27-JAN-1992
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Suh, Young J.
CC        REGISTRATION NUMBER:  P-41,337
CC        REFERENCE/DOCKET NUMBER:  27866/32760
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  (312) 474-6300
CC        TELEFAX:  (312) 474-0448
CC        TELEX:  (312) 474-6600
CC    INFORMATION FOR SEQ ID NO:  7:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  31 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  single
CC        TOPOLOGY:  linear
CC      MOLECULE TYPE:  DNA
SQ   SEQUENCE 31 BP; 7 A; 5 C; 5 G; 6 T; 8 OTHER.

  Query Match           40.7%;  Score 11;  DB 3;  Length 31;
  Best Local Similarity  38.5%;  Pred. No. 1.31e+03;
  Matches     5;  Conservative    7;  Mismatches   1;  Indels   0;  Gaps   0;

Db      17 YCTSACHMTBMGS 29
           :| :||::|::|:
Cp      25 TCAGACCCTGAGG 13


RESULT   30
ID   US-08-314-362-7 STANDARD; DNA; UNC; 31 BP.
AC   xxxxxx
DT
DE   Sequence 7, Application US/08314362
CC   Sequence 7, Application US/08314362
CC   Patent No. 5532127
CC    GENERAL INFORMATION:
CC      APPLICANT:  Gallatin, W. Michael
CC      APPLICANT:  Vazeux, Rosemay
CC      TITLE OF INVENTION:  I-CAM Related Protein
CC      NUMBER OF SEQUENCES:  22
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray &
CC        ADDRESSEE:  Bicknell
CC        STREET:  Two First National Plaza, 20 South Clark
CC        STREET:  Street
CC        CITY:  Chicago
CC        STATE:  Illinois
CC        COUNTRY:  USA
CC        ZIP:  60603
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, Version #1.25
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/314,362
CC        FILING DATE:
CC        CLASSIFICATION:  435
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  US/07/894,061
CC        FILING DATE:
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  US 07/827,689
CC        FILING DATE:  27-JAN-1992
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  US
CC        FILING DATE:  26-MAY-1992
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  No. 5532127and, Greta E.
CC        REGISTRATION NUMBER:  35,302
CC        REFERENCE/DOCKET NUMBER:  27866/30918
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  (312)346-5750
CC        TELEFAX:  (312)984-9740
CC        TELEX:  25-3856
CC    INFORMATION FOR SEQ ID NO:  7:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  31 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  single
CC        TOPOLOGY:  linear
CC      MOLECULE TYPE:  DNA
SQ   SEQUENCE 31 BP; 7 A; 5 C; 5 G; 6 T; 8 OTHER.

  Query Match           40.7%;  Score 11;  DB 1;  Length 31;
  Best Local Similarity  38.5%;  Pred. No. 1.31e+03;
  Matches     5;  Conservative    7;  Mismatches   1;  Indels   0;  Gaps   0;

Db      17 YCTSACHMTBMGS 29
           :| :||::|::|:
Cp      25 TCAGACCCTGAGG 13


Search completed: Mon Aug  2 12:06:16 1999
Job time : 82 secs.
```

Release 3.1A John F. Collins, Biocomputing Research Unit.

MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Mon Aug 2 11:45:28 1999; MasPar time 107.28 Seconds
589.719 Million cell updates/sec

Tabular output not generated.

Title: >US-09-121-239-23
Description: (1-27) from US09121239.seq
Perfect Score: 27
N.A. Sequence: 1 UCUGACUUUGAGCCUCAGGGUCUGAGU 27
Comp: AGACTGAAACTCGGAGTCCCAGACTCA

Scoring table: TABLE default
Gap 10

Nmatch STD : Dbase 0; Query 0

Searched: 2883791 seqs, 1171580779 bases x 2

Post-processing: Minimum Match 0%
Listing first 1000 summaries
Maximum DB seq length 50

Database: embl-est58
1:em_est10 2:em_est11 3:em_est17 4:em_est18 5:em_est2
6:em_est9 7:em_gss1
Database: genbank-est111
8:gb_est1 9:gb_est10 10:gb_est11 11:gb_est12 12:gb_est13
13:gb_est14 14:gb_est15 15:gb_est16 16:gb_est17
17:gb_est18 18:gb_est19 19:gb_est2 20:gb_est20
21:gb_est21 22:gb_est22 23:gb_est23 24:gb_est24
25:gb_est25 26:gb_est26 27:gb_est27 28:gb_est28
29:gb_est29 30:gb_est3 31:gb_est4 32:gb_est5 33:gb_est6
34:gb_est7 35:gb_est8 36:gb_est9 37:gb_gss1 38:gb_gss2
39:gb_gss3 40:gb_gss4 41:gb_gss5 42:gb_gss6

Statistics: Mean 7.131; Variance 1.539; scale 4.632

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.

No matches found.

Search completed: Mon Aug 2 11:56:07 1999
Job time : 639 secs.

****

MPSRCH (TM)

****

Release 3.1A John F. Collins, Biocomputing Research Unit.

MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Mon Aug 2 12:01:16 1999; MasPar time 106.49 Seconds
468.516 Million cell updates/sec

Tabular output not generated.

Title: >US-09-121-239-26
Description: (1-18) from US09121239.seq
Perfect Score: 18
N.A. Sequence: 1 GGAATCATCGAGGCATGG 18
Comp: CCTTAGTAGCTCCGTACC

Scoring table: TABLE default
Gap 10

Nmatch STD : Dbase 0; Query 0

Searched: 646147 seqs, 1385953633 bases x 2

Post-processing: Minimum Match 0%
Listing first 1000 summaries
Maximum DB seq length 50

Database: embl58
1:em_ba1 2:em_ba2 3:em_fun 4:em_htg 5:em_hum1 6:em_hum2
7:em_in 8:em_om 9:em_or 10:em_ov 11:em_pat 12:em_ph
13:em_pl 14:em_ro 15:em_sts 16:em_vi
Database: genbank111
17:gb_ba1 18:gb_ba2 19:gb_htg1 20:gb_htg2 21:gb_in1
22:gb_in2 23:gb_om 24:gb_ov 25:gb_pat 26:gb_ph 27:gb_pl1
28:gb_pl2 29:gb_pr1 30:gb_pr2 31:gb_pr3 32:gb_ro
33:gb_st 34:gb_sts 35:gb_sy 36:gb_un 37:gb_vi

Statistics: Mean 6.224; Variance 2.587; scale 2.406

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	13	72.2	37	25	I63515	Sequence 3 from patent	5.66e+02
2	13	72.2	37	25	I58617	Sequence 3 from patent	5.66e+02
c 3	12	66.7	23	25	AR008076	Sequence 2 from patent	2.17e+03

Note: Post-processor removed 997 summaries from list due to search parameters chosen.

ALIGNMENTS

RESULT 1
LOCUS I63515 37 bp DNA PAT 26-SEP-1997
DEFINITION Sequence 3 from patent US 5663070.
ACCESSION I63515
NID g2481088
VERSION I63515.1 GI:2481088
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 37)
AUTHORS Barr,P.J., Shapiro,J.P. and Kiefer,M.C.
TITLE Recombinant production of a soluble splice variant of the Fas (Apo-1) antigen, fas TM
JOURNAL Patent: US 5663070-A 3 02-SEP-1997;
FEATURES Location/Qualifiers
source 1. .37
/organism="unknown"
BASE COUNT 12 a 8 c 8 g 9 t
ORIGIN

Query Match 72.2%; Score 13; DB 25; Length 37;
Best Local Similarity 88.2%; Pred. No. 5.66e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Db      14 GGAATCATCAAGGAATG 30
           ||||||||| ||| |||
Qy       1 GGAATCATCGAGGCATG 17
```

RESULT 2
LOCUS I58617 37 bp DNA PAT 14-AUG-1997
DEFINITION Sequence 3 from patent US 5652210.
ACCESSION I58617
NID g2477855
VERSION I58617.1 GI:2477855
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 37)
AUTHORS Barr,P.J., Shapiro,J.P. and Kiefer,M.C.
TITLE Soluble splice variant of the Fas (APO-1) antigen, Fas.DELTA.TM
JOURNAL Patent: US 5652210-A 3 29-JUL-1997;
FEATURES Location/Qualifiers
source 1. .37
/organism="unknown"
BASE COUNT 12 a 8 c 8 g 9 t
ORIGIN

Query Match 72.2%; Score 13; DB 25; Length 37;
Best Local Similarity 88.2%; Pred. No. 5.66e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Db      14 GGAATCATCAAGGAATG 30
           ||||||||| ||| |||
Qy       1 GGAATCATCGAGGCATG 17
```

RESULT 3
LOCUS AR008076 23 bp DNA PAT 04-DEC-1998
DEFINITION Sequence 2 from patent US 5753432.
ACCESSION AR008076
NID g3967185
VERSION AR008076.1 GI:3967185
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 23)
AUTHORS Gudkov,A., Kazarov,A., Mazo,I. and Roninson,I.B.
TITLE Genes and genetic elements associated with control of neoplastic transformation in mammalian cells
JOURNAL Patent: US 5753432-A 2 19-MAY-1998;
FEATURES Location/Qualifiers
source 1. .23

/organism="unknown"
BASE COUNT 8 a 7 c 2 g 6 t
ORIGIN

Query Match 66.7%; Score 12; DB 25; Length 23;
Best Local Similarity 87.5%; Pred. No. 2.17e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Db       5 CCATCCATCGATGATT 20
           |||| | |||||||||
Cp      18 CCATGCCTCGATGATT 3
```

Search completed: Mon Aug 2 12:09:23 1999
Job time : 487 secs.

MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Mon Aug 2 12:15:12 1999; MasPar time 17.94 Seconds
214.980 Million cell updates/sec

Tabular output not generated.

Title: >US-09-121-239-26
Description: (1-18) from US09121239.seq
Perfect Score: 18
N.A. Sequence: 1 GGAATCATCGAGGCATGG 18
Comp: CCTTAGTAGCTCCGTACC

Scoring table: TABLE default
Gap 10

Nmatch STD : Dbase 0; Query 0

Searched: 271905 seqs, 107135622 bases x 2

Post-processing: Minimum Match 0%
Listing first 1000 summaries
Maximum DB seq length 50

Database: n-geneseq35
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33
34:part34 35:part35 36:part36 37:part37 38:part38
39:part39 40:part40 41:part41 42:part42 43:part43
44:part44 45:part45 46:part46 47:part47 48:part48
49:part49 50:part50 51:part51 52:part52 53:part53
54:part54 55:part55 56:part56 57:part57 58:part58
59:part59 60:part60

Statistics: Mean 4.989; Variance 2.549; scale 1.957

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
	1	13	72.2	37	15	Q93882	Fas intron 1 5' PCR p	7.01e+01
c	2	12	66.7	15	52	V60880	Mutagenic oligonucleo	2.56e+02
c	3	12	66.7	15	3	Q14334	MCPC 603 VH CDR3 walk	2.56e+02
	4	12	66.7	20	15	Q98678	Adaptor ATG-sense str	2.56e+02
c	5	12	66.7	23	15	Q98679	Adaptor ATG-antisense	2.56e+02
	6	12	66.7	24	2	Q11198	Proinsulin Ballast Co	2.56e+02
	7	12	66.7	27	28	T62501	Murine retrovirus con	2.56e+02
	8	12	66.7	30	2	Q11199	Proinsulin Ballast Co	2.56e+02
	9	11	61.1	21	56	V83708	Probe targeted to the	8.84e+02
c	10	11	61.1	22	49	V57714	Human chromosome 18 P	8.84e+02
	11	11	61.1	23	22	T31558	Ich-3 PCR primer cICE	8.84e+02
	12	11	61.1	23	14	Q79976	Human interleukin-1 b	8.84e+02
	13	11	61.1	25	32	T75952	DEN-2 cloning/sequenc	8.84e+02
	14	11	61.1	27	28	T62502	Murine retrovirus con	8.84e+02
	15	11	61.1	27	54	V72603	Peptide nucleic acid	8.84e+02
c	16	11	61.1	27	28	T62502	Murine retrovirus con	8.84e+02
	17	11	61.1	31	50	V67561	Nucleotide fragment c	8.84e+02
c	18	11	61.1	31	50	V67733	Nucleotide fragment c	8.84e+02
	19	11	61.1	37	41	V15733	Primer pINT 316b for	8.84e+02
	20	11	61.1	37	18	T03453	Human LAG-3 extracell	8.84e+02
c	21	11	61.1	37	41	V15732	Primer pINT 316a for	8.84e+02
c	22	11	61.1	41	51	V51130	Maize polymorphic mar	8.84e+02
c	23	11	61.1	41	46	V47878	Maize polymorphic sit	8.84e+02
c	24	10	55.6	19	59	V74222	CpG-N motif PCR prime	2.87e+03
c	25	10	55.6	27	60	V99504	T7 promoter/terminato	2.87e+03
c	26	10	55.6	27	6	Q36213	von Willebrand Factor	2.87e+03
c	27	10	55.6	48	7	Q46605	Mixed oligonucleotide	2.87e+03

Note: Post-processor removed 971 summaries from list due to search parameters chosen.

ALIGNMENTS

RESULT 1
ID Q93882 standard; cDNA; 37 BP.
AC Q93882;
DT 06-NOV-1995 (first entry)
DE Fas intron 1 5' PCR primer.
KW Fas-delta-TM; transmembrane deletion; apoptosis; antibody;
KW adoptive immunotherapy; transgenic animal; primer; PCR;
KW polymerase chain reaction; ss.
OS Synthetic.
PN WO9513701-A.
PD 26-MAY-1995.
PF 15-NOV-1994; U13173.
PR 15-NOV-1993; US-152443.
PA (LXRB-) LXR BIOTECHNOLOGY INC.
PI Barr PJ, Kiefer MC, Shapiro JP;
DR WPI; 95-200120/26.
PT New nucleic acid encoding Fas protein without its trans-membrane region
PT - and related vectors, transformed cells, transgenic animals, protein and
PT antibodies, useful for control of Fas mediated apoptosis
PS Example 2; Page 14; 38pp; English.
CC The intron-exon organization of the Fas transmembrane region was
CC determined by PCR. Primers were designed to flank each of the
CC putative introns, 1 and 2. The forward and reverse primers
CC flanking intron 1 are given in Q93882-83, and those for intron 2
CC in Q93884-85.
SQ Sequence 37 BP; 12 A; 8 C; 8 G; 9 T;

Query Match 72.2%; Score 13; DB 15; Length 37;
Best Local Similarity 88.2%; Pred. No. 7.01e+01;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 14 ggaatcatcgaggaatg 30
|||||||||| ||| |||
Qy 1 GGAATCATCGAGGCATG 17

RESULT 2
ID V60880 standard; DNA; 15 BP.
AC V60880;
DT 25-JAN-1999 (first entry)
DE Mutagenic oligonucleotide #2 for MAb MCPC603 Vh CDR3 coding sequence.
KW Mutation; mutagenesis; antigen-binding region; monoclonal antibody;
KW catalytic site; serine protease; complementarity determining region;
KW walk-through; ss.
OS Synthetic.
OS Homo sapiens.
PN US5798208-A.
PD 25-AUG-1998.

```
PF   02-NOV-1992; 930600.
PR   02-NOV-1992; US-930600.
PR   05-APR-1990; US-505314.
PA   (CREA/) CREA R.
PI   Crea R;
DR   WPI; 98-480376/41.
PT   Mutagenesis of pre-determined gene sequences - useful for systematic
PT   changes of pre-determined amino acids to see their effect on protein
PT   activity, and to create gene expression libraries
PS   Disclosure; Fig 8E; 33pp; English.
CC   The invention relates to a method of generating mutations in proteins by
CC   synthesising a mixture of oligonucleotides in order to alter the codons
CC   for specific amino acids within a defined region of the protein.  Using a
CC   range of oligonucleotides for the mutations, expression libraries of the
CC   mutant protein can be constructed.  As an example of the method, the
CC   antigen-binding region of the monoclonal antibody (MAb) MCPC603 (which
CC   binds phosphocholine) is altered to contain the catalytic triad residues
CC   for a serine protease.  Specifically the amino acids to be altered are
CC   selected from the Asp of the complementarity determining region (CDR) 1
CC   region of the variable heavy chain (Vh) of the antibody, the His of Vh
CC   CDR3 and the Ser of the CDR2 from the light chain variable region (Vl).
CC   The mutagenesis is by a "walk-through" method.  The sequence presented
CC   here corresponds to the degenerate mutagenic oligonucleotide used to
CC   construct an expression library encoding novel CDR3 sequences from the
CC   Vh region of the MAb (see V60862).
SQ   Sequence   15 BP;    0 A;    3 C;    0 G;    2 T;

  Query Match           66.7%;  Score 12;  DB 52;  Length 15;
  Best Local Similarity 35.7%;  Pred. No. 2.56e+02;
  Matches    5;  Conservative    8;  Mismatches   1;  Indels   0;  Gaps   0;

Db      2 rcbmcbmtvrtbmc 15
          :|: |::|::|::|
Cp     14 GCCTCGATGATTCC 1


RESULT    3
ID   Q14334 standard; DNA; 15 BP.
AC   Q14334;
DT   15-JAN-1992  (first entry)
DE   MCPC 603 VH CDR3 walk-through mutagenesis oligonucleotide (DHS).
KW   Mutagenesis; monoclonal antibody; Fv molecule; ss.
OS   Synthetic.
PN   WO9115581-A.
PD   17-OCT-1991.
PF   05-APR-1991; U02362.
PR   05-APR-1990; US-505314.
PA   (CREA/) CREA R.
PI   Crea R;
DR   WPI; 91-325224/44.
PT   Walk-through mutagenesis of proteins - by introducing predetermined
PT   amino acid in each sequence position in preselected region of the
PT   protein
PS   Disclosure; Fig 8E; 91pp; English.
CC   Walk-through mutagenesis of five out of six CDRs of the MCPC 603 Fv
CC   molecule is performed, and Asp, His and Ser are the preselected amino
CC   acids.  In this model, walk-through mutagenesis is carried out from two
CC   to three times with a different amino acid in a given region or domain.
CC   E.g., Ser and His are sequentially walked-through VL CDR1 (Q14330),
CC   and Asp and Ser are sequentially walked-through VL CDR3 (Q14331).
CC   VL CDR2 was not targeted for mutagenesis because structural studies
CC   indicated that this region contributes little to the binding site in
CC   MCPC 603.  In CDR1 of the VH chain of the Fv, Asp and His are walked
CC   through (Q14332).  Ser can be introduced at two positions in CDR1
CC   with a single base change.  In VH CDR2, His and Ser are the
CC   preselected amino acids used (Q14333) and in VH CDR3, Asp, His
CC   and Ser are each walked through the amino terminal five positions
CC   of CDR3.
CC   See also Q14321-34.
SQ   Sequence   15 BP;    0 A;    3 C;    0 G;    2 T;

  Query Match           66.7%;  Score 12;  DB 3;  Length 15;
  Best Local Similarity 35.7%;  Pred. No. 2.56e+02;
  Matches    5;  Conservative    8;  Mismatches   1;  Indels   0;  Gaps   0;

Db      2 rcbmcbmtvrtbmc 15
          :|: |::|::|::|
Cp     14 GCCTCGATGATTCC 1


RESULT    4
ID   Q98678 standard; DNA; 20 BP.
AC   Q98678;
DT   20-DEC-1995  (first entry)
DE   Adaptor ATG-sense strand.
KW   Genetic suppressor element; Tr6-GSE; fibroblast; transformation;
KW   retrovirus; tumor; cancer; gene therapy; adaptor; ss.
OS   Synthetic.
PN   WO9523855-A2.
PD   08-SEP-1995.
PF   01-MAR-1995; U02521.
PR   02-MAR-1994; US-204740.
PA   (UNII ) UNIV ILLINOIS FOUND.
PI   Gudkov A,  Kazarov A,  Mazo I,  Roninson IB;
DR   WPI; 95-320570/41.
PT   Isolation of genetic suppressor elements (GSEs) - useful in
PT   diagnostic assays for determining GSE mRNA expression levels and in
PT   the treatment of malignant cancers
PS   Example 1; Fig.1; 61pp; English.
CC   Poly-A+ RNA fragments obtd. from mouse fibroblast NIH3T3 cells were
CC   used to prepare double-stranded cDNA.  This was then ligated to an
CC   adaptor that provided ATG codons in all 3 reading frames, and was
CC   used to prepare a normalized random fragment cDNA library.
SQ   Sequence   20 BP;    6 A;    2 C;    7 G;    5 T;

  Query Match           66.7%;  Score 12;  DB 15;  Length 20;
  Best Local Similarity 87.5%;  Pred. No. 2.56e+02;
  Matches   14;  Conservative    0;  Mismatches   2;  Indels   0;  Gaps   0;

Db      1 aatcatcgatggatgg 16
          |||||||| | ||||
Qy      3 AATCATCGAGGCATGG 18


RESULT    5
ID   Q98679 standard; DNA; 23 BP.
AC   Q98679;
DT   20-DEC-1995  (first entry)
DE   Adaptor ATG-antisense strand.
KW   Genetic suppressor element; Tr6-GSE; fibroblast; transformation;
KW   retrovirus; tumor; cancer; gene therapy; adaptor; ss.
OS   Synthetic.
PN   WO9523855-A2.
PD   08-SEP-1995.
PF   01-MAR-1995; U02521.
PR   02-MAR-1994; US-204740.
PA   (UNII ) UNIV ILLINOIS FOUND.
PI   Gudkov A,  Kazarov A,  Mazo I,  Roninson IB;
DR   WPI; 95-320570/41.
PT   Isolation of genetic suppressor elements (GSEs) - useful in
PT   diagnostic assays for determining GSE mRNA expression levels and in
PT   the treatment of malignant cancers
PS   Example 1; Fig.1; 61pp; English.
CC   Poly-A+ RNA fragments obtd. from mouse fibroblast NIH3T3 cells were
CC   used to prepare double-stranded cDNA.  This was then ligated to an
CC   adaptor that provided ATG codons in all 3 reading frames, and was
CC   used to prepare a normalized random fragment cDNA library.
SQ   Sequence   23 BP;    8 A;    7 C;    2 G;    6 T;

  Query Match           66.7%;  Score 12;  DB 15;  Length 23;
  Best Local Similarity 87.5%;  Pred. No. 2.56e+02;
  Matches   14;  Conservative    0;  Mismatches   2;  Indels   0;  Gaps   0;

Db      5 ccatccatcgatgatt 20
          |||| | |||||||||
Cp     18 CCATGCCTCGATGATT 3
```

```
RESULT    6
ID   Q11198 standard; DNA; 24 BP.
AC   Q11198;
DT   05-JUN-1991  (first entry)
DE   Proinsulin Ballast Constituent-coding sequence #1.
KW   ballast constituent; fusion protein; oligonucleotide library;
KW   proinsulin; ss.
OS   Synthetic.
FH   Key             Location/Qualifiers
FT   repeat_unit     7..9
FT                   /*tag=  a
FT                   /note= "can be present 3 to 6 times"
PN   WO9103550-A.
PD   21-MAR-1991.
PF   28-AUG-1990; U04840.
PR   29-AUG-1989; US-399874.
PA   (FARH ) HOECHST AG.
PA   (GEHO-) GEN HOSPITAL CORP.
PI   Stengelin S, Ulmer W, Habermann P, Uhlmann E, Seed B;
DR   WPI; 91-102070/14.
PT   Prepn. of fusion proteins contg. ballast constituent and protein
PT   - giving prods. which are protease resistant or insoluble
PS   Claim 13; Page 51; 60pp; English.
CC   This oligonucleotide is an example of a member of an oligonucleotide
CC   library encoding ballast constituents. The oligonucleotides are
CC   inserted into a vector, functionally linked to a regulatory region
CC   and to the proinsulin structural gene. Host cells transformed with
CC   such plasmids produce proinsulin-ballast fusion proteins in
CC   high yield. The ballast is short and does not disturb the folding of
CC   the proinsulin. The fusion protein is soluble or easily
CC   solubilised. The oligonucleotide encodes a cleavage site at its 3'
CC   end which allows easy removal of the ballast constituent.
CC   See also Q11194-7 and Q11199-Q11202.
SQ   Sequence   24 BP;    2 A;    6 C;    5 G;    1 T;

 Query Match           66.7%;  Score 12;  DB 2;  Length 24;
 Best Local Similarity  42.9%;  Pred. No. 2.56e+02;
 Matches    6;  Conservative    7;  Mismatches   1;  Indels   0;  Gaps   0;

Db      9 ddcddcddcdaggc 22
          :: ::|::|:|||| 
Qy      1 GGAATCATCGAGGC 14


RESULT    7
ID   T62501 standard; DNA; 27 BP.
AC   T62501;
DT   28-APR-1997  (first entry)
DE   Murine retrovirus consensus left side integration response sequence.
KW   Consensus sequence; left side; integration response; LTR;
KW   long terminal repeat; retroviral attachment sequence; preparation;
KW   gene delivery construct; ss.
OS   Murine retrovirus.
PN   WO9626745-A1.
PD   06-SEP-1996.
PF   28-FEB-1996; U02877.
PR   28-FEB-1995; US-395355.
PA   (UYCR-) UNIV CREIGHTON.
PI   Hodgson CP;
DR   WPI; 96-412589/41.
PT   Gene delivery system including liposome or dendrimer and
PT   perpetuation molecule  - esp. for gene therapy, provides efficient
PT   and stable expression of chimeric genes more safely than use of
PT   viruses.
PS   Example 3; Fig 2; 50pp; English.
CC   The present sequence is the murine retrovirus consensus left side
CC   (U3) integration response sequence, which reads into the long
CC   terminal repeat (LTR). It can be used as a retroviral attachment
CC   sequence in the preparation of a gene delivery construct.
SQ   Sequence   27 BP;    4 A;    0 C;    1 G;    1 T;

 Query Match           66.7%;  Score 12;  DB 28;  Length 27;
 Best Local Similarity   0.0%;  Pred. No. 2.56e+02;
 Matches    0;  Conservative   13;  Mismatches   4;  Indels   0;  Gaps   0;

Db      7 rrwbvvhrvhndnhndk 23
          ::::::: :: : : :: 
Qy      2 GAATCATCGAGGCATGG 18


RESULT    8
ID   Q11199 standard; DNA; 30 BP.
AC   Q11199;
DT   05-JUN-1991  (first entry)
DE   Proinsulin Ballast Constituent-coding sequence #2.
KW   ballast constituent; fusion protein; oligonucleotide library;
KW   proinsulin; ss.
OS   Synthetic.
FH   Key             Location/Qualifiers
FT   repeat_unit     7..9
FT                   /*tag=  a
FT                   /note= "may be present 3 to 6 times"
PN   WO9103550-A.
PD   21-MAR-1991.
PF   28-AUG-1990; U04840.
PR   29-AUG-1989; US-399874.
PA   (FARH ) HOECHST AG.
PA   (GEHO-) GEN HOSPITAL CORP.
PI   Stengelin S, Ulmer W, Habermann P, Uhlmann E, Seed B;
DR   WPI; 91-102070/14.
PT   Prepn. of fusion proteins contg. ballast constituent and protein
PT   - giving prods. which are protease resistant or insoluble
PS   Claim 13; Page 51; 60pp; English.
CC   This oligonucleotide is an example of a member of an oligonucleotide
CC   library encoding ballast constituents. The oligonucleotides are
CC   inserted into a vector, functionally linked to a regulatory region
CC   and to the proinsulin structural gene. Host cells transformed with
CC   such plasmids produce proinsulin-ballast fusion proteins in
CC   high yield. The ballast is short and does not disturb the folding of
CC   the proinsulin. The fusion protein is soluble or easily
CC   solubilised. The oligonucleotide encodes a cleavage site at its 3'
CC   end which allows easy removal of the ballast constituent.
CC   See also Q11194-8 and Q11200-Q11202.
SQ   Sequence   30 BP;    2 A;    8 C;    6 G;    1 T;

 Query Match           66.7%;  Score 12;  DB 2;  Length 30;
 Best Local Similarity  42.9%;  Pred. No. 2.56e+02;
 Matches    6;  Conservative    7;  Mismatches   1;  Indels   0;  Gaps   0;

Db     15 ddcddcddcdaggc 28
          :: ::|::|:|||| 
Qy      1 GGAATCATCGAGGC 14


RESULT    9
ID   V83708 standard; DNA; 21 BP.
AC   V83708;
DT   26-FEB-1999  (first entry)
DE   Probe targeted to the 5.8S rDNA gene.
KW   Internal transcribed spacer 2; ITS2; probe; Aspergillus flavus;
KW   A. niger; A. terreus; A. nidulans; Fusarium solani; F. moniliforme;
KW   Mucor rouxii; M  racemosus; M. plumbeus; M. indicus; A. fumigatus;
KW   M. circinilloides f. circinelloides; Rhizopus oryzae; R. microsporus;
KW   R. circinans; R. stolonifer; Rhizomucor pusillus; Absidia corymbifera;
KW   Cunninghamella elegans; Pseudallescheria boydii; Scedosporium apiospermum;
KW   Penicillium notatum; Sporothrix schenkii; filamentous fungus; ss.
OS   Synthetic.
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /note= "labelled with biotin"
PN   WO9850584-A2.
PD   12-NOV-1998.
PF   01-MAY-1998; U08926.
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PR   02-MAY-1997; US-045400.
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PI   Aidorevich L, Choi JS, Morrison CJ, Reiss E;
DR   WPI; 99-034737/03.
PT   New nucleic acid probes for filamentous fungi - for detecting e.g.
PT   Aspergillus, Fusarium, Mucor, Rhizopus, Rhizomucor, Absidia,
PT   Cunninghamella, Pseudoallescheria boydii, Penicillium and Sporothrix
PT   species.
PS   Claim 48; Page 22; 45pp; English.
CC   Probes V83677-708 are derived from the internal transcribed spacer 2
CC   (ITS2) region of various filamentous fungi (see V70845-73). The probes
CC   are species-specific, and can be used for identifying a species selected
CC   from Aspergillus flavus, A. fumigatus, A. niger, A. terreus, A. nidulans,
CC   Fusarium solani, F. moniliforme, Mucor rouxii, M. racemosus, M. plumbeus,
CC   M. indicus, M. circinilloides f. circinelloides, Rhizopus oryzae,
CC   R. microsporus, R. circinans, R. stolonifer, Rhizomucor pusillus,
CC   Absidia corymbifera, Cunninghamella elegans, Pseudallesheria boydii
CC   (teleomorph of Scedosporium apiospermum), Penicillium notatum, or
CC   Sporothrix schenkii. The probes can be used for differentiating
CC   filamentous fungal species from each other and from other medically
CC   important fungi.
SQ   Sequence   21 BP;    6 A;    4 C;    4 G;    6 T;

  Query Match           61.1%;  Score 11;  DB 56;  Length 21;
  Best Local Similarity  90.9%;  Pred. No. 8.84e+02;
  Matches    10;  Conservative    1;  Mismatches   0;  Indels   0;  Gaps   0;

Db      1 gaatcatcgar 11
          ||||||||||:
Qy      2 GAATCATCGAG 12


RESULT   10
ID   V57714 standard; DNA; 22 BP.
AC   V57714;
DT   18-NOV-1998  (first entry)
DE   Human chromosome 18 PCR mapping primer clone 7r.
KW   Manic-depressive illness; susceptibility; genotype; diagnosis;
KW   chromosomal marker; polymorphic marker; chromosome 18; human;
KW   myo-inositol monophosphatase protein; IMP-18p; PCR primer; ss.
OS   Synthetic.
OS   Homo sapiens.
PN   WO9818963-A1.
PD   07-MAY-1998.
PF   28-OCT-1997; U19381.
PR   28-OCT-1996; US-029278.
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PI   Badner JA, Berrettini WH, Detera-Wadleigh SD, Esterling LE,
PI   Gershon ES, Goldin LR, Sanders AR, Yoshikawa T;
DR   WPI; 98-272247/24.
PT   New isolated IMP.18p myo-inositol monophosphatase - used to develop
PT   products for determining susceptibility to manic depressive illness
PT   and as targets for preventive and therapeutic treatments
PS   Example 5; Page 71; 118pp; English.
CC   A method has been developed for determining a genotype associated with
CC   increased susceptibility to manic-depressive (MD) illness. The method
CC   comprises determining the genotype of an affected individual with at
CC   least one polymorphic marker localised within the chromosomal region
CC   defined by and including markers D18S843 and D18S869 and determining the
CC   genotype associated with increased susceptibility to MD disorder. The
CC   method can be used for determining susceptibility to MD illness
CC   including bipolar disorder, genetic counselling of individuals from
CC   families affected with MD illness, and aid in the differential diagnosis
CC   of MD illness from other psychiatric pathologies. Products from the
CC   present invention can also be used to obtain modulators of IMP.18p myo-
CC   inositol monophosphatase protein activity and as targets for preventive
CC   and therapeutic treatments. The present sequence represents a PCR primer
CC   used in the mapping of human chromosome 18 for determining the genotype
CC   of MD illness susceptibility, used in an example from the present
CC   invention.
SQ   Sequence   22 BP;    7 A;    3 C;    6 G;    6 T;

  Query Match           61.1%;  Score 11;  DB 49;  Length 22;
  Best Local Similarity 100.0%;  Pred. No. 8.84e+02;
  Matches    11;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db      7 gcctcgatgat 17
          ||||||||||:
Cp     14 GCCTCGATGAT 4


RESULT   11
ID   T31558 standard; DNA; 23 BP.
AC   T31558;
DT   25-SEP-1996  (first entry)
DE   Ich-3 PCR primer cICEAs.
KW   Ich-3; ICE-ced-3 homologue; programmed cell death; apoptosis;
KW   interleukin-1 beta converting enzyme; gene therapy; primer; PCR;
KW   polymerase chain reaction; ss.
OS   Synthetic.
PN   WO9620721-A1.
PD   11-JUL-1996.
PF   04-JAN-1996; U00177.
PR   04-JAN-1995; US-368704.
PA   (GEHO ) GEN HOSPITAL CORP.
PI   Miura M,  Yuan J;
DR   WPI; 96-333763/33.
PT   Preventing or promoting programmed cell death in vertebrate cells -
PT   comprises inhibiting or increasing the activity of
PT   interleukin-1-beta converting enzyme, or altering expression of
PT   other related genes
PS   Disclosure; Page 24; 127pp; English.
CC   PCR primers cICEB (T31557) and cICEAs (T31558) were used to
CC   amplify cDNA from embryonic day 14 mouse brain cDNA.  cDNA
CC   (T31554) coding for a novel homologue, Ich-3 (R98464), of
CC   interleukin-1 beta converting enzyme was isolated.  This can
CC   be used in methods of controlling programmed cell death.
SQ   Sequence   23 BP;    5 A;    5 C;    6 G;    4 T;

  Query Match           61.1%;  Score 11;  DB 22;  Length 23;
  Best Local Similarity  78.6%;  Pred. No. 8.84e+02;
  Matches    11;  Conservative    1;  Mismatches   2;  Indels   0;  Gaps   0;

Db      4 athatccaggcntg 17
          ||:||| |||| ||
Qy      4 ATCATCGAGGCATG 17


RESULT   12
ID   Q79976 standard; DNA; 23 BP.
AC   Q79976;
DT   13-SEP-1995  (first entry)
DE   Human interleukin-1 beta convering enzyme Ice-4 PCR primer cTceAs.
KW   Human interleukin-1 beta converitng enzyme homolog; Ice-4;
KW   oncogene bcl-2; programmed cell death; cancer treatment;
KW   PCR primer cTceAs; ss.
OS   Synthetic.
PN   WO9500160-A.
PD   05-JAN-1995.
PF   10-JUN-1994; U06630.
PR   24-JUN-1993; US-080850.
PA   (GEHO ) GEN HOSPITAL CORP.
PI   Miura M,  Yuan J;
DR   WPI; 95-051742/07.
PT   Promoting or preventing programmed cell death in vertebrate cells
PT   - by inhibiting the activity of interleukin-1 beta converting
PT   enzyme.
PS   Disclosure; Page 22; 116pp; English.
CC   Q79975 and Q79976 are a pair of primers for the PCR amplification
CC   of Q79969, which encodes R66769 human interleukin-1 beta converting
CC   enzyme homolog (Ice-4), increasing Ice-4s enzymatic activity can
CC   promote the programmed cell death of cancer cells (pref. those
CC   overexpressing the bcl-2 oncogene), this can be used as the basis
CC   of a new cancer treatment. Alternatively by reducing Ice-4s enzymatic
CC   activity programmed cell death can be inhibited, this may be useful
CC   in the development of new cell lines which remain viable in culture
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CC   for extended or indefinite periods, independant of growth factors.
SQ   Sequence   23 BP;     5 A;     5 C;     6 G;     4 T;

  Query Match           61.1%;  Score 11;  DB 14;  Length 23;
  Best Local Similarity  78.6%;  Pred. No. 8.84e+02;
  Matches    11;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Db       4 athatccaggcntg 17
           ||:||| |||| ||
Qy       4 ATCATCGAGGCATG 17


RESULT   13
ID   T75952 standard; DNA; 25 BP.
AC   T75952;
DT   15-SEP-1997  (first entry)
DE   DEN-2 cloning/sequencing sense primer, D2-2702.
KW   Dengue 2 virus; polyprotein; capsid; prM; M; E; NS1; NS2A; NS2B; NS3;
KW   NS4A; NS4B; NS5; PDK-53; quadravalent vaccine; immunity; serotype;
KW   chimeric DEN-2/1 virus; chimeric DEN-2/3 virus; chimeric DEN-2/4 virus;
KW   dengue fever; fatal dengue haemorrhagic fever; dengue shock syndrome;
KW   DHF; DSS; PCR; amplify; polymerase chain reaction; primer; ss.
OS   Synthetic.
PN   WO9640933-A1.
PD   19-DEC-1996.
PF   06-JUN-1996; U09209.
PR   07-JUN-1995; US-483292.
PA   (UYMA-) UNIV MAHIDOL AT SALAYA.
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PI   Bhamarapravati N,  Butrapet S,  Chang J,  Gubler DJ;
PI   Halstead SB,  Kinney R, Trent DW;
DR   WPI; 97-052330/05.
PT   PDK-53, a clone of infectious attenuated Dengue 2 virus strain 16681
PT   - also chimeric DEN-2/1, DEN-2/3 and DEN-1/4 viruses, used as a
PT   quadravalent vaccine for protecting against Dengue virus infection
PS   Examples; Page 101; 261pp; English.
CC   The sequences given in T75909-T76029 are primers which were used in
CC   the amplification, cloning and sequencing of the Dengue-2 viral cDNA's
CC   of the invention.  The Dengue 2 viral DNA encodes a polyprotein which
CC   comprises the capsid, prM, M, E, NS1, NS2A, NS2B, NS3, NS4A, NS4B and
CC   NS5 proteins.  The quadravalent vaccine of the invention comprises an
CC   attenuated Dengue virus clone, PDK-53, and a chimeric DEN-2/1 virus,
CC   a chimeric DEN-2/3 virus, and/or a chimeric DEN-2/4 virus.  The new
CC   quadravalent vaccines are used to protect against infection by all
CC   four serotypes of dengue virus, DEN-1, DEN-2, DEN-3 and DEN-4, which
CC   can lead to dengue fever or fatal dengue haemorrhagic fever/dengue
CC   shock syndrome (DHF/DSS). Host cells are used to produce the recombinant
CC   protein products of the DNA constructs which are used in the
CC   vaccines.
SQ   Sequence   25 BP;     11 A;     4 C;     8 G;     2 T;

  Query Match           61.1%;  Score 11;  DB 32;  Length 25;
  Best Local Similarity  86.7%;  Pred. No. 8.84e+02;
  Matches    13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Db       3 ggaatcatgcaggca 17
           ||||||||  |||||
Qy       1 GGAATCATCGAGGCA 15


RESULT   14
ID   T62502 standard; DNA; 27 BP.
AC   T62502;
DT   28-APR-1997  (first entry)
DE   Murine retrovirus consensus right side integration response sequence.
KW   Consensus sequence; right side; integration response; LTR;
KW   long terminal repeat; retroviral attachment sequence; preparation;
KW   gene delivery construct; ss.
OS   Murine retrovirus.
PN   WO9626745-A1.
PD   06-SEP-1996.
PF   28-FEB-1996; U02877.
PR   28-FEB-1995; US-395355.
PA   (UYCR-) UNIV CREIGHTON.
PI   Hodgson CP;
DR   WPI; 96-412589/41.
PT   Gene delivery system including liposome or dendrimer and
PT   perpetuation molecule  - esp. for gene therapy, provides efficient
PT   and stable expression of chimeric genes more safely than use of
PT   viruses.
PS   Example 3; Fig 2; 50pp; English.
CC   The present sequence is the murine retrovirus consensus right side
CC   (U5) integration response sequence, which reads towards the outside
CC   of the long terminal repeat (LTR). It can be used as a retroviral
CC   attachment sequence in the preparation of a gene delivery construct.
SQ   Sequence   27 BP;     1 A;     2 C;     0 G;     6 T;

  Query Match           61.1%;  Score 11;  DB 28;  Length 27;
  Best Local Similarity  0.0%;  Pred. No. 8.84e+02;
  Matches     0;  Conservative   12;  Mismatches    1;  Indels    0;  Gaps    0;

Db       6 sbshhbhyyvrrr 18
           :: ::::::::::
Qy       1 GGAATCATCGAGG 13


RESULT   15
ID   V72603 standard; DNA; 27 BP.
AC   V72603;
DT   11-FEB-1999  (first entry)
DE   Peptide nucleic acid molecule #3.
KW   peptide nucleic acid; PNA; 2-dimensional; 3-dimensional; nanometer;
KW   geometric structure; supramolecular; computer chip; conductive;
KW   insulator; robot arm; network; ss.
OS   Synthetic.
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /note= "attached to a hydrogen group"
FT   modified_base   27
FT                   /*tag=  b
FT                   /note= "attached to an amide group"
PN   EP-881228-A2.
PD   02-DEC-1998.
PF   26-MAY-1998; 109492.
PR   30-MAY-1997; EP-108670.
PA   (BOEF ) BOEHRINGER MANNHEIM GMBH.
PI   Batz H, Hansen HF, Koch T;
DR   WPI; 99-001349/01.
PT   Constructing defined oligo- or polymeric geometric structure -
PT   useful for preparation of fine networks in nanometer size.
PS   Example 2; Page 9; 12pp; English.
CC   The present invention describes a method for constructing a defined
CC   oligo- or polymeric geometric structure. The method comprises combining
CC   a first oligomeric element having bound recognition elements with a
CC   second oligomeric element having bound recognition elements capable of
CC   recognising the recognition elements of the first unit under binding
CC   conditions. The recognition elements are heterocyclic moieties
CC   recognising other elements by hydrogen bonding, van-der-Waals
CC   interaction, pi -stacking or water exclusion (the recognition elements
CC   of at least one oligomeric element are bound to space defined locations
CC   of a nucleic acid analogue). The geometric structures are useful for the
CC   preparation of fine networks in nanometer size, e.g. for the conduct
CC   networks of computer chips, robot arms of nanometer scale and new
CC   materials and polymers with conductivity and/or insulator properties.
CC   The present sequence represents a peptide nucleic acid molecule used in
CC   an example from the present invention for the assembly of a double fork
CC   geometric structure containing 6 nucleic acid analogues.
SQ   Sequence   27 BP;     7 A;     6 C;     8 G;     6 T;

  Query Match           61.1%;  Score 11;  DB 54;  Length 27;
  Best Local Similarity  82.4%;  Pred. No. 8.84e+02;
  Matches    14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Db       9 ggtagcatcgatgcatg 25
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Qy      1 GGAATCATCGAGGCATG 17


RESULT   16
ID   T62502 standard; DNA; 27 BP.
AC   T62502;
DT   28-APR-1997  (first entry)
DE   Murine retrovirus consensus right side integration response sequence.
KW   Consensus sequence; right side; integration response; LTR;
KW   long terminal repeat; retroviral attachment sequence; preparation;
KW   gene delivery construct; ss.
OS   Murine retrovirus.
PN   WO9626745-A1.
PD   06-SEP-1996.
PF   28-FEB-1996; U02877.
PR   28-FEB-1995; US-395355.
PA   (UYCR-) UNIV CREIGHTON.
PI   Hodgson CP;
DR   WPI; 96-412589/41.
PT   Gene delivery system including liposome or dendrimer and
PT   perpetuation molecule - esp. for gene therapy, provides efficient
PT   and stable expression of chimeric genes more safely than use of
PT   viruses.
PS   Example 3; Fig 2; 50pp; English.
CC   The present sequence is the murine retrovirus consensus right side
CC   (U5) integration response sequence, which reads towards the outside
CC   of the long terminal repeat (LTR). It can be used as a retroviral
CC   attachment sequence in the preparation of a gene delivery construct.
SQ   Sequence   27 BP;    1 A;    2 C;    0 G;    6 T;

  Query Match           61.1%;  Score 11;  DB 28;  Length 27;
  Best Local Similarity  0.0%;  Pred. No. 8.84e+02;
  Matches    0;  Conservative   11;  Mismatches   0;  Indels   0;  Gaps   0;

Db      7 bshhbhyyvrr 17
          ::::::::::
Cp     18 CCATGCCTCGA 8


RESULT   17
ID   V67561 standard; DNA; 31 BP.
AC   V67561;
DT   21-DEC-1998  (first entry)
DE   Nucleotide fragment containing polymorphic site, WI-15260.
KW   ss; polymorphic site; nucleic acid analysis; diagnosis; monitoring;
KW   cancer; inflammation; heart disease; CNS disease.
OS   Homo sapiens.
PN   WO9838846-A2.
PD   11-SEP-1998.
PF   06-MAR-1998; U04571.
PR   28-MAR-1997; US-042125.
PR   07-MAR-1997; US-813159.
PA   (AFFY-) AFFYMETRIX INC.
PI   Berno A, Chee M, Fan J, Lipshutz RJ;
DR   WPI; 98-495419/42.
PT   New nucleic acid segments containing polymorphic sites, or
PT   complements and methods of detecting a nucleic acid - for general
PT   use including diagnosis and monitoring of diseases
PS   Claim 1; Page 15; 42pp; English.
CC   New nucleic acid segment comprising one of the 10 - 100 bp sequences
CC   given in the specification (sequences of a polymorphic site), or the
CC   complement of the segment and a method of analysing a nucleic acid
CC   comprising determining the base occupying the polymorphic site of the
CC   polymorphic fragment sequences are disclosed in the specification.  The
CC   information obtained from nucleic acid analysis by the method described
CC   is useful in diagnosis or monitoring of diseases like cancer,
CC   inflammation, heart disease, CNS diseases, and susceptibility to
CC   infection by microorganisms. In addition, the nucleic acid segments are
CC   useful in manufacturing medication in the treatment of prophylaxis of
CC   diseases, and also the use of the DNA segments as pharmaceutical.
SQ   Sequence   31 BP;    9 A;    7 C;    9 G;    5 T;

  Query Match           61.1%;  Score 11;  DB 50;  Length 31;
  Best Local Similarity  84.6%;  Pred. No. 8.84e+02;
  Matches   11;  Conservative    1;  Mismatches   1;  Indels   0;  Gaps   0;

Db      7 aatcatggargca 19
          |||||| ||:|||
Qy      3 AATCATCGAGGCA 15


RESULT   18
ID   V67733 standard; DNA; 31 BP.
AC   V67733;
DT   24-DEC-1998  (first entry)
DE   Nucleotide fragment containing polymorphic site, WI-5836.
KW   ss; polymorphic site; nucleic acid analysis; diagnosis; monitoring;
KW   cancer; inflammation; heart disease; CNS disease.
OS   Homo sapiens.
PN   WO9838846-A2.
PD   11-SEP-1998.
PF   06-MAR-1998; U04571.
PR   28-MAR-1997; US-042125.
PR   07-MAR-1997; US-813159.
PA   (AFFY-) AFFYMETRIX INC.
PI   Berno A, Chee M, Fan J, Lipshutz RJ;
DR   WPI; 98-495419/42.
PT   New nucleic acid segments containing polymorphic sites, or
PT   complements and methods of detecting a nucleic acid - for general
PT   use including diagnosis and monitoring of diseases
PS   Claim 1; Page 21; 42pp; English.
CC   New nucleic acid segment comprising one of the 10 - 100 bp sequences
CC   given in the specification (sequences of a polymorphic site), or the
CC   complement of the segment and a method of analysing a nucleic acid
CC   comprising determining the base occupying the polymorphic site of the
CC   polymorphic fragment sequences are disclosed in the specification.  The
CC   information obtained from nucleic acid analysis by the method described
CC   is useful in diagnosis or monitoring of diseases like cancer,
CC   inflammation, heart disease, CNS diseases, and susceptibility to
CC   infection by microorganisms. In addition, the nucleic acid segments are
CC   useful in manufacturing medication in the treatment of prophylaxis of
CC   diseases, and also the use of the DNA segments as pharmaceutical.
SQ   Sequence   31 BP;    12 A;    4 C;    3 G;    11 T;

  Query Match           61.1%;  Score 11;  DB 50;  Length 31;
  Best Local Similarity  76.5%;  Pred. No. 8.84e+02;
  Matches   13;  Conservative    1;  Mismatches   3;  Indels   0;  Gaps   0;

Db      2 catgattcaatgatycc 18
          ||||  || |||||:||
Cp     17 CATGCCTCGATGATTCC 1


RESULT   19
ID   V15733 standard; DNA; 37 BP.
AC   V15733;
DT   26-JUN-1998  (first entry)
DE   Primer pINT 316b for insulin analogue preparation.
KW   Insulin analogue; histidine-rich B-chain domain; treatment;
KW   diabetes; zinc-binding; delayed release; PCR primer;
KW   subcutaneous administration; ss.
OS   Synthetic.
OS   Homo sapiens.
PN   EP-821006-A2.
PD   28-JAN-1998.
PF   17-JUL-1997; 112197.
PR   26-JUL-1996; DE-030242.
PA   (FARH ) HOECHST AG.
PI   Ertl J, Geisen K, Habermann P, Seipke G;
DR   WPI; 98-102618/10.
PT   Insulin analogues with histidine-rich B-chain domain - with high
PT   zinc-complexing capacity, useful for treatment of diabetes
PS   Example 3; Page 7; 22pp; German.
CC   The present sequence was used in the preparation of insulin
CC   analogues with a histidine-rich B-chain domain, which can be used in
CC   pharmaceutical formulations for treating diabetes. The analogues
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CC   have a greater zinc-binding capacity than conventional forms of
CC   insulin, forming stable complexes having delayed release properties
CC   on subcutaneous administration.
SQ   Sequence   37 BP;    8 A;    13 C;    12 G;    4 T;

  Query Match           61.1%;  Score 11;  DB 41;  Length 37;
  Best Local Similarity  92.3%;  Pred. No. 8.84e+02;
  Matches   12;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db     18 atcatcgcggcat 30
          ||||||| |||||
Qy      4 ATCATCGAGGCAT 16


RESULT   20
ID   T03453 standard; DNA; 37 BP.
AC   T03453;
DT   14-JUN-1996  (first entry)
DE   Human LAG-3 extracellular domain D1 amplification primer.
KW   Immunoglobulin extracellular domain; Ig superfamily; membrane protein;
KW   soluble; LAG-3; immunosuppression; MHC class II; binding; target;
KW   natural killer; NK cell; activated T lymphocyte; CD4-related; ss.
OS   Synthetic.
PN   WO9530750-A2.
PD   16-NOV-1995.
PF   05-MAY-1995; F00593.
PR   06-MAY-1994; FR-005643.
PA   (ISTF ) ARS APPLIED RES SYST HOLDING NV.
PA   (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
PA   (INSR ) INST ROUSSY GUSTAVE.
PI   Faure F,  Hercend T,  Huard B,  Triebel F;
DR   WPI; 95-404117/51.
PT   New soluble polypeptide contg. extracellular domains of LAG-3  -
PT   useful as immunosuppressant and to generate antibodies for use as
PT   immunostimulants
PS   Example 3; Page 18; 69pp; French.
CC   Soluble polypeptides comprising at least part of one of the four
CC   Ig-like extracellular domains of LAG-3 (see R87089) are claimed.
CC   The sol. polypeptides bind to MHC class II molecules, making them
CC   useful as immunosuppressants or, when coupled to a toxin or radio-
CC   isotope, for targetted destruction of cells which express MHC class
CC   II molecules (e.g. leukaemia or melanoma cells). Antibodies to the
CC   polypeptides act as immunostimulants. The present sequence is that
CC   of a PCR primer used for amplifying DNA coding for domain D1
CC   of LAG-3 for inclusion in an expression vector.
SQ   Sequence   37 BP;    6 A;    13 C;    13 G;    5 T;

  Query Match           61.1%;  Score 11;  DB 18;  Length 37;
  Best Local Similarity  92.3%;  Pred. No. 8.84e+02;
  Matches   12;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db     14 catcgaggcctgg 26
          ||||||||| |||
Qy      6 CATCGAGGCATGG 18


RESULT   21
ID   V15732 standard; DNA; 37 BP.
AC   V15732;
DT   26-JUN-1998  (first entry)
DE   Primer pINT 316a for insulin analogue preparation.
KW   Insulin analogue; histidine-rich B-chain domain; treatment;
KW   diabetes; zinc-binding; delayed release; PCR primer;
KW   subcutaneous administration; ss.
OS   Synthetic.
OS   Homo sapiens.
PN   EP-821006-A2.
PD   28-JAN-1998.
PF   17-JUL-1997; 112197.
PR   26-JUL-1996; DE-030242.
PA   (FARH ) HOECHST AG.
PI   Ertl J, Geisen K, Habermann P, Seipke G;
DR   WPI; 98-102618/10.
PT   Insulin analogues with histidine-rich B-chain domain - with high
PT   zinc-complexing capacity, useful for treatment of diabetes
PS   Example 3; Page 7; 22pp; German.
CC   The present sequence was used in the preparation of insulin
CC   analogues with a histidine-rich B-chain domain, which can be used in
CC   pharmaceutical formulations for treating diabetes. The analogues
CC   have a greater zinc-binding capacity than conventional forms of
CC   insulin, forming stable complexes having delayed release properties
CC   on subcutaneous administration.
SQ   Sequence   37 BP;    4 A;    8 C;    16 G;    9 T;

  Query Match           61.1%;  Score 11;  DB 41;  Length 37;
  Best Local Similarity  92.3%;  Pred. No. 8.84e+02;
  Matches   12;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db      2 atgccgcgatgat 14
          ||||| |||||||
Cp     16 ATGCCTCGATGAT 4


RESULT   22
ID   V51130 standard; DNA; 41 BP.
AC   V51130;
DT   11-JAN-1999  (first entry)
DE   Maize polymorphic marker S26G5/G6-3 DNA.
KW   Polymorphic marker; allele-specific; primer; probe; amplification;
KW   hybridisation; plant; hybrid certification; genetic contribution;
KW   progeny; back-cross; hybrid; ancestry; maize; ss.
OS   Zea mays.
FH   Key             Location/Qualifiers
FT   variation       21
FT                   /*tag= a
FT                   /replace= "a"
FT                   /note= "polymorphism"
PN   WO9824796-A1.
PD   11-JUN-1998.
PF   01-DEC-1997; U21782.
PR   07-MAR-1997; US-813507.
PR   02-DEC-1996; US-032069.
PA   (AFFY-) AFFYMETRIX INC.
PI   Landry BS, Lemieux B, Murigneux A, Sapolsky RJ;
DR   WPI; 98-333252/29.
PT   Brassica species allele-specific oligonucleotide probes and primers
PT   - useful for plant breeding
PS   Claim 1; Page 46; 65pp; English.
CC   This DNA sequence is a region of a Zea mays genome which contains a
CC   polymorphic marker. This sequence can be used in the construction of
CC   allele-specific primers and probes for amplification or hybridisation,
CC   e.g. to determine common or disparate ancestry between 2 or more plants,
CC   to monitor the genetic contribution of an ancestral plant, to trace the
CC   progeny of proprietary plants, in certification of a hybrid plant or to
CC   identify the progeny of a back-crossed plant with an ancestral plant.
SQ   Sequence   41 BP;    11 A;    9 C;    9 G;    12 T;

  Query Match           61.1%;  Score 11;  DB 51;  Length 41;
  Best Local Similarity  86.7%;  Pred. No. 8.84e+02;
  Matches   13;  Conservative    0;  Mismatches   2;  Indels   0;  Gaps   0;

Db     15 tgcccagatgattcc 29
          ||||  |||||||||
Cp     15 TGCCTCGATGATTCC 1


RESULT   23
ID   V47878 standard; DNA; 41 BP.
AC   V47878;
DT   14-OCT-1998  (first entry)
DE   Maize polymorphic site oligonucleotide marker UMC59-G5/G6-3.
KW   Maize; marker; probe; PCR primer; polymorphism; vegetal sequence;
KW   polymorphic site; corn; graminae species; ss.
OS   Synthetic.
OS   Zea sp.
PN   WO9830717-A2.
```

PD 16-JUL-1998.
PF 02-DEC-1997; E07134.
PR 02-DEC-1996; US-032069.
PA (BIOC-) BIOCEM SA.
PI Murigneux A;
DR WPI; 98-399160/34.
PT Vegetal sequences including single nucleotide polymorphism - useful,
PT e.g. to determine polymorphisms in plants, determine strain in plant
PT breeding and to correlate polymorphisms with phenotypic traits
PS Claim 2; Page 14; 32pp; English.
CC The present invention describes a nucleic acid segment comprising at
CC least 10 contiguous nucleotides from a vegetal sequence including a
CC polymorphic site which is a single nucleotide polymorphism (SNP), or the
CC complement of the segment. Also described are: (1) an allele-specific
CC oligonucleotides hybridising to segment, or their complements, and (2) a
CC method of analysing nucleic acids from a subject, by determining if a
CC base is occupying any one (or a set) of polymorphic sites in 261
CC sequences derived from six maize lines (see V47701 to V47961). The
CC segments are useful in fingerprint analysis in plants to determine which
CC polymorphisms are present, which strain a plant belongs to and to
CC distinguish between strains. The polymorphisms may correlate with
CC phenotypic traits (e.g. plant growth rate or crop yield), and the
CC segments are useful to determine the presence/absence of specific
CC polymorphisms correlating with the existence/absence of particular
CC traits. The segments are also useful in marker assisted back-cross
CC techniques to select plants with a higher percentage of recurrent parent
CC in a back-cross population. Segments incorporate SNPs which occur more
CC frequently than other polymorphism types and are therefore more likely to
CC be located close to genetic loci of interest; different forms of
CC characterised SNPs are also often easier to detect than other
CC polymorphism types.
SQ Sequence 41 BP; 11 A; 9 C; 8 G; 12 T;

Query Match 61.1%; Score 11; DB 46; Length 41;
Best Local Similarity 80.0%; Pred. No. 8.84e+02;
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 15 tgcccaratgattcc 29
|||| :||||||||
Cp 15 TGCCTCGATGATTCC 1

RESULT 24
ID V74222 standard; DNA; 19 BP.
AC V74222;
DT 15-MAR-1999 (first entry)
DE CpG-N motif PCR primer Mu-15F.
KW CpG-N motif; immunostimulation; antigen; CpG-S motif; immunisation;
KW viral antigen; bacterial antigen; parasite; therapeutic; growth factor;
KW toxins; tumour suppressor; cytokine; apoptotic protein; interferon;
KW hormone; clotting factor; ligand; receptor; PCR primer; ss.
OS Synthetic.
PN WO9852581-A1.
PD 26-NOV-1998.
PF 20-MAY-1998; U10408.
PR 20-MAY-1997; US-047233.
PR 20-MAY-1997; US-047209.
PA (OTTA-) OTTAWA CIVIC HOSPITAL LOEB RES INST.
PA (QIAG-) QIAGEN GMBH.
PA (IOWA-) UNIV IOWA RES FOUND.
PI Davis HL, Krieg AM, Schorr J, Wu T;
DR WPI; 99-059712/05.
PT Use of neutralising CpG and stimulating CpG motifs in DNA vectors -
PT for enhancing the immunostimulatory effect of an antigen or
PT enhancing the expression of a therapeutic polypeptide
PS Example 1; Page 58; 109pp; English.
CC V74209-V74236 are PCR primers used to describe a method for enhancing the
CC immunostimulatory effect of an antigen encoded by nucleic acid contained
CC in a nucleic acid construct. The method involves determining the CpG-N
CC and CpG-S motifs present in the construct, removing neutralising CpG
CC (CpG-N) motifs and optionally inserting stimulatory CpG (CpG-S) motifs in
CC the construct, thereby producing a nucleic acid construct having enhanced
CC immunostimulatory efficacy. The method can be used for immunisation
CC against viral antigens, e.g. from hepatitis B virus (HBV), bacterial
CC antigens or an antigen derived from a parasite. They can also be used
CC for expression of a therapeutic polypeptide, e.g. growth factors, toxins,
CC tumour suppressors, cytokines, apoptotic proteins, interferons, hormones,
CC clotting factors, ligands and receptors.
SQ Sequence 19 BP; 1 A; 7 C; 5 G; 6 T;

Query Match 55.6%; Score 10; DB 59; Length 19;
Best Local Similarity 85.7%; Pred. No. 2.87e+03;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 3 gcctcgacgtttcc 16
||||||| | ||||
Cp 14 GCCTCGATGATTCC 1

RESULT 25
ID V99504 standard; DNA; 27 BP.
AC V99504;
DT 29-MAR-1999 (first entry)
DE T7 promoter/terminator PCR primer SM79.
KW Lysine; transgenic plant; seed storage protein; vector; pSK5;
KW phage T7; promoter; terminator; PCR; primer; ss.
OS Synthetic.
OS Bacteriophage T7.
PN WO9842831-A2.
PD 01-OCT-1998.
PF 27-MAR-1998; U06051.
PR 27-MAR-1997; US-824627.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
PI Epelbaum SU, Falco SC, McDevitt RE;
DR WPI; 99-045139/04.
PT Nucleic acids and chimeric genes for increasing seed lysine content
PT - comprise sequence encoding all or part of lysine ketoglutarate
PT reductase, useful to improve nutritional quality of seeds from
PT transformed plants
PS Example 21; Page 100; 231pp; English.
CC PCR primers SM79 and SM78 (see V99504) are designed to prime a
CC 300 base fragment from pBT430 spanning the T7 promoter and
CC terminator sequences. This fragment was used in the construction
CC of expression vector pSK5. Chimeric genes for lysine-rich
CC synthetic seed storage proteins suitable for expression in the
CC seeds of plants have been constructed in pSK5 (see V99513-18,
CC V99527-32, V99539-41). The invention also provides claimed
CC nucleic acids and chimeric genes useful for improving the
CC nutritional quality of seeds from transgenic plants. Methods
CC involve manipulation of lysine ketoglutarate reductase and
CC lysine-insensitive dihydrodipicolinic acid synthase activity (see
CC W87757-66).
SQ Sequence 27 BP; 6 A; 8 C; 8 G; 5 T;

Query Match 55.6%; Score 10; DB 60; Length 27;
Best Local Similarity 81.3%; Pred. No. 2.87e+03;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 8 atgccacgatgcgtcc 23
||||| |||| |||
Cp 16 ATGCCTCGATGATTCC 1

RESULT 26
ID Q36213 standard; DNA; 27 BP.
AC Q36213;
DT 25-MAY-1993 (first entry)
DE von Willebrand Factor cDNA PCR primer.
KW von Willebrand Factor; vascular disorders; prevention; treatment;
KW platelet aggregation; induction; inhibition; thrombosis;
KW polymerase chain reaction; ss.
OS Synthetic.
PN WO9300357-A.
PD 07-JAN-1993.
PF 29-JUN-1992; U05172.
PR 28-JUN-1991; US-720588.

```
PA   (RHON ) RHONE POULENC RORER INT HOLDIN.
PA   (SCRI ) SCRIPPS RES INST.
PI   Chang MN, McGarry DG, Regan JR, Ruggeri ZM, Ware JL;
DR   WPI; 93-036328/04.
PT   Compsn. contg. polypeptide derived from Von=Willebrand factor
PT   sub-unit - competing with Von=Willebrand factor for GPIB
PT   receptors useful for prevention and treatment of vascular disorders,
PT   e.g. thrombosis
PS   Example; Page 67; 174pp; English.
CC   The sequence is that of a primer used in the synthesis by PCR of a
CC   vWF fragment contg., 5' to 3', a SalI site, a consensus initiation
CC   sequence, an initiating methionine codon, the codon sequence for
CC   the signal peptide, and approximately, the first 100 codons of the
CC   vWF propeptide followed by an XbaI site.
SQ   Sequence   27 BP;    6 A;    10 C;    6 G;    5 T;

  Query Match           55.6%;  Score 10;  DB 6;  Length 27;
  Best Local Similarity  85.7%;  Pred. No. 2.87e+03;
  Matches    12;  Conservative    0;  Mismatches   2;  Indels   0;  Gaps   0;

Db       7 gccaccatgattcc 20
           ||| | ||||||||
Cp      14 GCCTCGATGATTCC 1


RESULT   27
ID   Q46605 standard; DNA; 48 BP.
AC   Q46605;
DT   20-DEC-1993  (first entry)
DE   Mixed oligonucleotide (9a) encodes ballast constituent.
KW   Fusion protein; ballast constituent; monkey pro-insulin;
KW   recombinant protein production; HMG CoA reductase;
KW   human 3-hydroxy-3-methylglutaryl-coenzyme A-reductase;
KW   mixed oligonucleotide; ss.
OS   Synthetic.
PN   US5227293-A.
PD   13-JUL-1993.
PF   29-AUG-1989; 399874.
PR   29-AUG-1989; US-399874.
PR   23-APR-1992; US-838221.
PA   (GEHO ) GEN HOSPITAL CORP.
PA   (FARH ) HOECHST AG.
PI   Habermann P,  Seed B,  Stengelin S,  Uhlmann E,  Ulmer W;
DR   WPI; 93-235119/29.
PT   Fusion proteins for prodn. of e.g. pro-insulin - comprise gene
PT   for desired protein and oligo-nucleotide(s) encoding ballast
PT   protein
PS   Example 1; Column 7; 22pp; English.
CC   Mixed oligonucleotide (9) (Q46604) encodes a ballast constituent
CC   and forms part of a fusion gene with the monkey pro-insulin gene;
CC   the double-stranded ballast constituent insert was prepared from
CC   the synthetic mixed oligonucleotide (9a) (Q46605) which was filled
CC   in with Klenow polymerase and cut with MluI and Nco. The genebank
CC   pINT4x contains the resulting plasmid population. After transforming
CC   E.coli WS3110 with the genebank, one clone (pINT41) was found to
CC   produce, in relatively large quantities, a protein containing an
CC   insulin constituent. The exact sequence of the pINT41 ballast
CC   constituent is given in Q51798.
SQ   Sequence   48 BP;    3 A;    9 C;    16 G;    7 T;

  Query Match           55.6%;  Score 10;  DB 7;  Length 48;
  Best Local Similarity  35.7%;  Pred. No. 2.87e+03;
  Matches     5;  Conservative    7;  Mismatches   2;  Indels   0;  Gaps   0;

Db       4 gcgthghhghhghh 17
           || |:|::|:: ::
Cp      14 GCCTCGATGATTCC 1


Search completed: Mon Aug  2 12:19:19 1999
Job time : 247 secs.
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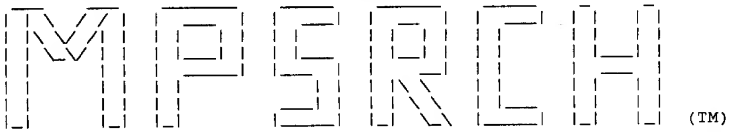

****

Release 3.1A John F. Collins, Biocomputing Research Unit.

MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Mon Aug 2 12:13:30 1999; MasPar time 6.97 Seconds
183.116 Million cell updates/sec

Tabular output not generated.

Title: >US-09-121-239-26
Description: (1-18) from US09121239.seq
Perfect Score: 18
N.A. Sequence: 1 GGAATCATCGAGGCATGG 18
Comp: CCTTAGTAGCTCCGTACC

Scoring table: TABLE default
Gap 10

Nmatch STD : Dbase 0; Query 0

Searched: 137068 seqs, 35432894 bases x 2

Post-processing: Minimum Match 0%
Listing first 1000 summaries
Maximum DB seq length 50

Database: n-issued
1:5A_COMB 2:5B_COMB 3:5C_COMB 4:PCT9_COMB 5:backfiles1

Statistics: Mean 4.750; Variance 2.219; scale 2.140

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
	1	13	72.2	37	2	US-08-152-	Sequence 3, Applicatio	1.08e+01
	2	13	72.2	37	2	US-08-444-	Sequence 3, Applicatio	1.08e+01
	3	12	66.7	20	4	PCT-US95-0	Sequence 1, Applicatio	4.58e+01
	4	12	66.7	20	3	US-08-204-	Sequence 1, Applicatio	4.58e+01
	5	12	66.7	20	2	US-08-480-	Sequence 13, Applicati	4.58e+01
	6	12	66.7	20	4	PCT-US95-0	Sequence 1, Applicatio	4.58e+01
c	7	12	66.7	23	2	US-08-480-	Sequence 14, Applicati	4.58e+01
c	8	12	66.7	23	3	US-08-204-	Sequence 2, Applicatio	4.58e+01
c	9	12	66.7	23	4	PCT-US95-0	Sequence 2, Applicatio	4.58e+01
c	10	12	66.7	23	4	PCT-US95-0	Sequence 2, Applicatio	4.58e+01
	11	11	61.1	26	4	PCT-US94-0	Sequence 87, Applicati	1.83e+02
	12	11	61.1	27	1	US-08-463-	Sequence 37, Applicati	1.83e+02
	13	11	61.1	27	4	PCT-US93-1	Sequence 7, Applicatio	1.83e+02
	14	11	61.1	27	1	US-07-998-	Sequence 37, Applicati	1.83e+02
	15	11	61.1	27	1	US-08-462-	Sequence 37, Applicati	1.83e+02
	16	11	61.1	27	4	PCT-US92-1	Sequence 37, Applicati	1.83e+02
c	17	11	61.1	33	4	PCT-US94-0	Sequence 2, Applicatio	1.83e+02
c	18	11	61.1	33	3	US-08-455-	Sequence 6, Applicatio	1.83e+02
c	19	11	61.1	33	4	PCT-US94-0	Sequence 6, Applicatio	1.83e+02
	20	11	61.1	42	5	5164485-3	Patent No. 5164485.	1.83e+02
	21	10	55.6	15	1	US-08-311-	Sequence 176, Applicat	6.87e+02
	22	10	55.6	15	1	US-08-311-	Sequence 9, Applicatio	6.87e+02
c	23	10	55.6	20	1	US-07-855-	Sequence 12, Applicati	6.87e+02
c	24	10	55.6	20	1	US-07-969-	Sequence 12, Applicati	6.87e+02
c	25	10	55.6	21	4	PCT-US96-0	Sequence 61, Applicati	6.87e+02
c	26	10	55.6	21	3	US-08-479-	Sequence 61, Applicati	6.87e+02
c	27	10	55.6	23	1	US-08-181-	Sequence 11, Applicati	6.87e+02
c	28	10	55.6	27	3	US-08-474-	Sequence 19, Applicati	6.87e+02
c	29	10	55.6	27	1	US-08-182-	Sequence 12, Applicati	6.87e+02
c	30	10	55.6	27	4	PCT-US92-0	Sequence 12, Applicati	6.87e+02
c	31	10	55.6	28	2	US-08-626-	Sequence 12, Applicati	6.87e+02
c	32	10	55.6	28	1	US-08-146-	Sequence 30, Applicati	6.87e+02
c	33	10	55.6	28	1	US-08-146-	Sequence 29, Applicati	6.87e+02
c	34	10	55.6	28	3	US-08-693-	Sequence 13, Applicati	6.87e+02
	35	10	55.6	29	3	US-08-655-	Sequence 9, Applicatio	6.87e+02
c	36	10	55.6	30	3	US-08-897-	Sequence 8, Applicatio	6.87e+02
c	37	10	55.6	33	1	US-08-138-	Sequence 7, Applicatio	6.87e+02
	38	10	55.6	35	4	PCT-US94-0	Sequence 1, Applicatio	6.87e+02
	39	10	55.6	35	3	US-08-491-	Sequence 1, Applicatio	6.87e+02
c	40	10	55.6	35	4	PCT-US94-0	Sequence 5, Applicatio	6.87e+02
c	41	10	55.6	35	3	US-08-455-	Sequence 5, Applicatio	6.87e+02
c	42	10	55.6	35	4	PCT-US94-0	Sequence 1, Applicatio	6.87e+02
c	43	10	55.6	40	1	US-08-141-	Sequence 14, Applicati	6.87e+02

Note: Post-processor removed 957 summaries from list due to search parameters chosen.

ALIGNMENTS

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RESULT    1
ID   US-08-152-443A-3 STANDARD; DNA; UNC; 37 BP.
AC   xxxxxx
DT
DE   Sequence 3, Application US/08152443A
CC   Sequence 3, Application US/08152443A
CC   Patent No. 5663070
CC    GENERAL INFORMATION:
CC      APPLICANT:  BARR, PHILIP J.
CC      APPLICANT:  SHAPIRO, JOHN P.
CC      APPLICANT:  KIEFER, MICHAEL C.
CC      TITLE OF INVENTION:  NOVEL FAS PROTEIN AND METHODS OF USE
CC      TITLE OF INVENTION:  THEREOF
CC      NUMBER OF SEQUENCES:  22
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  MORRISON & FOERSTER
CC        STREET:  755 Page Mill Road
CC        CITY:  Palo Alto
CC        STATE:  California
CC        COUNTRY:  USA
CC        ZIP:  94304-1018
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, Version #1.30
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/152,443A
CC        FILING DATE:  15-NOV-1993
CC        CLASSIFICATION:  435
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  LEHNHARDT, SUSAN K.
CC        REGISTRATION NUMBER:  33,943
CC        REFERENCE/DOCKET NUMBER:  23647-20006.00
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  (415) 813-5600
CC        TELEFAX:  (415) 494-0792
CC        TELEX:  706141
CC     INFORMATION FOR SEQ ID NO:  3:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  37 base pairs
CC         TYPE:  nucleic acid
CC         STRANDEDNESS:  single
```

```
CC       TOPOLOGY:  linear
SQ   SEQUENCE 37 BP; 12 A; 8 C; 8 G; 9 T; 0 OTHER.

  Query Match           72.2%;  Score 13;  DB 2;  Length 37;
  Best Local Similarity  88.2%;  Pred. No. 1.08e+01;
  Matches   15;  Conservative    0;  Mismatches   2;  Indels   0;  Gaps   0;

Db     14 GGAATCATCAAGGAATG 30
          ||||||||| ||| |||
Qy      1 GGAATCATCGAGGCATG 17


RESULT    2
ID   US-08-444-231-3 STANDARD; DNA; UNC; 37 BP.
AC   xxxxxx
DT
DE   Sequence 3, Application US/08444231
CC   Sequence 3, Application US/08444231
CC   Patent No. 5652210
CC    GENERAL INFORMATION:
CC      APPLICANT:  BARR, PHILIP J.
CC      APPLICANT:  SHAPIRO, JOHN P.
CC      APPLICANT:  KIEFER, MICHAEL C.
CC      TITLE OF INVENTION:  NOVEL FAS PROTEIN AND METHODS OF USE
CC      TITLE OF INVENTION:  THEREOF
CC      NUMBER OF SEQUENCES:  22
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  MORRISON & FOERSTER
CC        STREET:  755 Page Mill Road
CC        CITY:  Palo Alto
CC        STATE:  California
CC        COUNTRY:  USA
CC        ZIP:  94304-1018
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, Version #1.30
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/444,231
CC        FILING DATE:  18-MAY-1995
CC        CLASSIFICATION:  530
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  US 08/152,443
CC        FILING DATE:  15-NOV-1993
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  LEHNHARDT, SUSAN K.
CC        REGISTRATION NUMBER:  33,943
CC        REFERENCE/DOCKET NUMBER:  23647-20006.00
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  (415) 813-5600
CC        TELEFAX:  (415) 494-0792
CC        TELEX:  706141
CC    INFORMATION FOR SEQ ID NO:  3:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  37 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  single
CC        TOPOLOGY:  linear
SQ   SEQUENCE 37 BP; 12 A; 8 C; 8 G; 9 T; 0 OTHER.

  Query Match           72.2%;  Score 13;  DB 2;  Length 37;
  Best Local Similarity  88.2%;  Pred. No. 1.08e+01;
  Matches   15;  Conservative    0;  Mismatches   2;  Indels   0;  Gaps   0;

Db     14 GGAATCATCAAGGAATG 30
          ||||||||| ||| |||
Qy      1 GGAATCATCGAGGCATG 17


RESULT    3
ID   PCT-US95-02521-1 STANDARD; DNA; UNC; 20 BP.
AC   xxxxxx
DT
DE   Sequence 1, Application PC/TUS9502521
CC   Sequence 1, Application PC/TUS9502521
CC    GENERAL INFORMATION:
CC      APPLICANT:
CC      TITLE OF INVENTION:  Methods for Identifying Genetic
CC      TITLE OF INVENTION:  Suppressor Elements and Genes Associated with Malignant
CC      TITLE OF INVENTION:  Growth in Cancer Cells
CC      NUMBER OF SEQUENCES:  13
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  PCT/US95/02521
CC        FILING DATE:
CC    INFORMATION FOR SEQ ID NO:  1:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  20 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  single
CC        TOPOLOGY:  linear
CC      MOLECULE TYPE:  cDNA
SQ   SEQUENCE 20 BP; 6 A; 2 C; 7 G; 5 T; 0 OTHER.

  Query Match           66.7%;  Score 12;  DB 4;  Length 20;
  Best Local Similarity  87.5%;  Pred. No. 4.58e+01;
  Matches   14;  Conservative    0;  Mismatches   2;  Indels   0;  Gaps   0;

Db      1 AATCATCGATGGATGG 16
          ||||||||| | ||||
Qy      3 AATCATCGAGCCATGG 18


RESULT    4
ID   US-08-204-740-1 STANDARD; DNA; UNC; 20 BP.
AC   xxxxxx
DT
DE   Sequence 1, Application US/08204740
CC   Sequence 1, Application US/08204740
CC   Patent No. 5753432
CC    GENERAL INFORMATION:
CC      APPLICANT:  Gudkov, Andrei
CC      APPLICANT:  Kazarov, Alexander
CC      APPLICANT:  Mazo, Ilya
CC      APPLICANT:  Roninson, Igor B
CC      TITLE OF INVENTION:  Methods for Identifying Genetic
CC      TITLE OF INVENTION:  Suppressor Elements and Genes Associated with Malignant
CC      TITLE OF INVENTION:  Growth in Cancer Cells
CC      NUMBER OF SEQUENCES:  13
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Allgretti & Witcoff, Ltd.
CC        STREET:  10 S. Wacker Drive, Suite 3000
CC        CITY:  Chicago
CC        STATE:  Illinois
CC        COUNTRY:  USA
CC        ZIP:  60606
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, Version #1.25
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/204,740
CC        FILING DATE:  04-MAR-1994
CC        CLASSIFICATION:  435
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  No. 5753432nan, Kevin E
CC        REGISTRATION NUMBER:  35,303
CC        REFERENCE/DOCKET NUMBER:  93,354-C
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  312-715-1000
```

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CC        TELEFAX:  312-715-1234
CC        TELEX:  910-221-5317
CC    INFORMATION FOR SEQ ID NO:  1:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  20 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  single
CC        TOPOLOGY:  linear
CC      MOLECULE TYPE:  cDNA
SQ   SEQUENCE 20 BP; 6 A; 2 C; 7 G; 5 T; 0 OTHER.

  Query Match           66.7%;  Score 12;  DB 3;  Length 20;
  Best Local Similarity  87.5%;  Pred. No. 4.58e+01;
  Matches    14;  Conservative    0;  Mismatches   2;  Indels   0;  Gaps   0;

Db      1 AATCATCGATGGATGG 16
          |||||||||  | ||||
Qy      3 AATCATCGAGGCATGG 18


RESULT    5
ID   US-08-480-552-13 STANDARD; DNA; UNC; 20 BP.
AC   xxxxxx
DT
DE   Sequence 13, Application US/08480552
CC   Sequence 13, Application US/08480552
CC   Patent No. 5665550
CC    GENERAL INFORMATION:
CC      APPLICANT:  Gudkov, Andrei
CC      APPLICANT:  Roninson, Igor B.
CC      TITLE OF INVENTION:  Genes And Genetic Elements Associated
CC      TITLE OF INVENTION:  With Sensitivity To Chemotherapeutic Drugs
CC      NUMBER OF SEQUENCES:  22
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Allegretti & Witcoff, Ltd.
CC        STREET:  75 State Street
CC        CITY:  Boston
CC        STATE:  Massachusetts
CC        COUNTRY:  U.S.A.
CC        ZIP:  02109
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, Version #1.25
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/480,552
CC        FILING DATE:  07-JUN-1995
CC        CLASSIFICATION:  435
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  US 08/033,086
CC        FILING DATE:  09 MAR 1993
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Keown, Wayne A.
CC        REGISTRATION NUMBER:  33,923
CC        REFERENCE/DOCKET NUMBER:  93,354
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  617/345-9100
CC        TELEFAX:  617/345-9111
CC    INFORMATION FOR SEQ ID NO:  13:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  20 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  single
CC        TOPOLOGY:  linear
CC      MOLECULE TYPE:  cDNA
CC      HYPOTHETICAL:  NO
CC      ANTI-SENSE:  NO
SQ   SEQUENCE 20 BP; 6 A; 2 C; 7 G; 5 T; 0 OTHER.

  Query Match           66.7%;  Score 12;  DB 2;  Length 20;
  Best Local Similarity  87.5%;  Pred. No. 4.58e+01;
  Matches    14;  Conservative    0;  Mismatches   2;  Indels   0;  Gaps   0;

Db      1 AATCATCGATGGATGG 16
          |||||||||  | ||||
Qy      3 AATCATCGAGGCATGG 18


RESULT    6
ID   PCT-US95-02303-1 STANDARD; DNA; UNC; 20 BP.
AC   xxxxxx
DT
DE   Sequence 1, Application PC/TUS9502303
CC   Sequence 1, Application PC/TUS9502303
CC    GENERAL INFORMATION:
CC      APPLICANT:
CC      TITLE OF INVENTION:  Genes and Genetic Elements Associated
CC      TITLE OF INVENTION:  with Sensitivity to Cisplatin
CC      NUMBER OF SEQUENCES:  25
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  PCT/US95/02303
CC    INFORMATION FOR SEQ ID NO:  1:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  20 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  single
CC        TOPOLOGY:  linear
CC      MOLECULE TYPE:  cDNA
SQ   SEQUENCE 20 BP; 6 A; 2 C; 7 G; 5 T; 0 OTHER.

  Query Match           66.7%;  Score 12;  DB 4;  Length 20;
  Best Local Similarity  87.5%;  Pred. No. 4.58e+01;
  Matches    14;  Conservative    0;  Mismatches   2;  Indels   0;  Gaps   0;

Db      1 AATCATCGATGGATGG 16
          |||||||||  | ||||
Qy      3 AATCATCGAGGCATGG 18


RESULT    7
ID   US-08-480-552-14 STANDARD; DNA; UNC; 23 BP.
AC   xxxxxx
DT
DE   Sequence 14, Application US/08480552
CC   Sequence 14, Application US/08480552
CC   Patent No. 5665550
CC    GENERAL INFORMATION:
CC      APPLICANT:  Gudkov, Andrei
CC      APPLICANT:  Roninson, Igor B.
CC      TITLE OF INVENTION:  Genes And Genetic Elements Associated
CC      TITLE OF INVENTION:  With Sensitivity To Chemotherapeutic Drugs
CC      NUMBER OF SEQUENCES:  22
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Allegretti & Witcoff, Ltd.
CC        STREET:  75 State Street
CC        CITY:  Boston
CC        STATE:  Massachusetts
CC        COUNTRY:  U.S.A.
CC        ZIP:  02109
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, Version #1.25
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/480,552
CC        FILING DATE:  07-JUN-1995
CC        CLASSIFICATION:  435
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  US 08/033,086
```

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CC         FILING DATE:  09 MAR 1993
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Keown, Wayne A.
CC         REGISTRATION NUMBER:  33,923
CC         REFERENCE/DOCKET NUMBER:  93,354
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  617/345-9100
CC         TELEFAX:  617/345-9111
CC     INFORMATION FOR SEQ ID NO:  14:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  23 base pairs
CC         TYPE:  nucleic acid
CC         STRANDEDNESS:  single
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  cDNA
CC       HYPOTHETICAL:  NO
CC       ANTI-SENSE:  YES
SQ   SEQUENCE 23 BP; 8 A; 7 C; 2 G; 6 T; 0 OTHER.

  Query Match           66.7%;  Score 12;  DB 2;  Length 23;
  Best Local Similarity  87.5%;  Pred. No. 4.58e+01;
  Matches    14;  Conservative    0;  Mismatches   2;  Indels   0;  Gaps   0;

Db       5 CCATCCATCGATGATT 20
           |||| | |||||||||
Cp      18 CCATGCCTCGATGATT 3


RESULT    8
ID   US-08-204-740-2 STANDARD; DNA; UNC; 23 BP.
AC   xxxxxx
DT
DE   Sequence 2, Application US/08204740
CC   Sequence 2, Application US/08204740
CC   Patent No. 5753432
CC    GENERAL INFORMATION:
CC      APPLICANT:  Gudkov, Andrei
CC      APPLICANT:  Kazarov, Alexander
CC      APPLICANT:  Mazo, Ilya
CC      APPLICANT:  Roninson, Igor B
CC      TITLE OF INVENTION:  Methods for Identifying Genetic
CC      TITLE OF INVENTION:  Suppressor Elements and Genes Associated with Malignant
CC      TITLE OF INVENTION:  Growth in Cancer Cells
CC      NUMBER OF SEQUENCES:  13
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Allgretti & Witcoff, Ltd.
CC        STREET:  10 S. Wacker Drive, Suite 3000
CC        CITY:  Chicago
CC        STATE:  Illinois
CC        COUNTRY:  USA
CC        ZIP:  60606
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, Version #1.25
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/204,740
CC        FILING DATE:  04-MAR-1994
CC        CLASSIFICATION:  435
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  No. 5753432nan, Kevin E
CC        REGISTRATION NUMBER:  35,303
CC        REFERENCE/DOCKET NUMBER:  93,354-C
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  312-715-1000
CC        TELEFAX:  312-715-1234
CC        TELEX:  910-221-5317
CC    INFORMATION FOR SEQ ID NO:  2:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  23 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  single
CC        TOPOLOGY:  linear
CC      MOLECULE TYPE:  cDNA
SQ   SEQUENCE 23 BP; 8 A; 7 C; 2 G; 6 T; 0 OTHER.

  Query Match           66.7%;  Score 12;  DB 3;  Length 23;
  Best Local Similarity  87.5%;  Pred. No. 4.58e+01;
  Matches    14;  Conservative    0;  Mismatches   2;  Indels   0;  Gaps   0;

Db       5 CCATCCATCGATGATT 20
           |||| | |||||||||
Cp      18 CCATGCCTCGATGATT 3


RESULT    9
ID   PCT-US95-02521-2 STANDARD; DNA; UNC; 23 BP.
AC   xxxxxx
DT
DE   Sequence 2, Application PC/TUS9502521
CC   Sequence 2, Application PC/TUS9502521
CC    GENERAL INFORMATION:
CC      APPLICANT:
CC      TITLE OF INVENTION:  Methods for Identifying Genetic
CC      TITLE OF INVENTION:  Suppressor Elements and Genes Associated with Malignant
CC      TITLE OF INVENTION:  Growth in Cancer Cells
CC      NUMBER OF SEQUENCES:  13
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  PCT/US95/02521
CC        FILING DATE:
CC    INFORMATION FOR SEQ ID NO:  2:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  23 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  single
CC        TOPOLOGY:  linear
CC      MOLECULE TYPE:  cDNA
SQ   SEQUENCE 23 BP; 8 A; 7 C; 2 G; 6 T; 0 OTHER.

  Query Match           66.7%;  Score 12;  DB 4;  Length 23;
  Best Local Similarity  87.5%;  Pred. No. 4.58e+01;
  Matches    14;  Conservative    0;  Mismatches   2;  Indels   0;  Gaps   0;

Db       5 CCATCCATCGATGATT 20
           |||| | |||||||||
Cp      18 CCATGCCTCGATGATT 3


RESULT   10
ID   PCT-US95-02303-2 STANDARD; DNA; UNC; 23 BP.
AC   xxxxxx
DT
DE   Sequence 2, Application PC/TUS9502303
CC   Sequence 2, Application PC/TUS9502303
CC    GENERAL INFORMATION:
CC      APPLICANT:
CC      TITLE OF INVENTION:  Genes and Genetic Elements Associated
CC      TITLE OF INVENTION:  with Sensitivity to Cisplatin
CC      NUMBER OF SEQUENCES:  25
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  PCT/US95/02303
CC    INFORMATION FOR SEQ ID NO:  2:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  23 base pairs
CC        TYPE:  nucleic acid
```

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CC       STRANDEDNESS:  single
CC       TOPOLOGY:  linear
CC     MOLECULE TYPE:  cDNA
SQ   SEQUENCE 23 BP; 8 A; 7 C; 2 G; 6 T; 0 OTHER.

  Query Match           66.7%;  Score 12;  DB 4;  Length 23;
  Best Local Similarity  87.5%;  Pred. No. 4.58e+01;
  Matches    14;  Conservative    0;  Mismatches   2;  Indels   0;  Gaps   0;

Db      5 CCATCCATCGATGATT 20
          |||| | |||||||||
Cp     18 CCATGCCTCGATGATT 3


RESULT   11
ID   PCT-US94-03437-87 STANDARD; DNA; UNC; 26 BP.
AC   xxxxxx
DT
DE   Sequence 87, Application PC/TUS9403437
CC   Sequence 87, Application PC/TUS9403437
CC    GENERAL INFORMATION:
CC      APPLICANT:
CC      APPLICANT:
CC      TITLE OF INVENTION:  HOMOGENEOUS IMMUNOASSAYS USING MUTANT
CC      TITLE OF INVENTION:  GLUCOSE-6-PHOSPHATE DEHYDROGENASES
CC      NUMBER OF SEQUENCES:  124
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  PCT/US94/03437
CC        FILING DATE:
CC    INFORMATION FOR SEQ ID NO:  87:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  26 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  single
CC        TOPOLOGY:  linear
CC      MOLECULE TYPE:  DNA (genomic)
CC      HYPOTHETICAL:  NO
CC      ANTI-SENSE:  NO
CC      ORIGINAL SOURCE:
CC        ORGANISM:  Leuconostoc mesenteroides
CC        STRAIN:  ATCC 12291
SQ   SEQUENCE 26 BP; 4 A; 8 C; 8 G; 6 T; 0 OTHER.

  Query Match           61.1%;  Score 11;  DB 4;  Length 26;
  Best Local Similarity  92.3%;  Pred. No. 1.83e+02;
  Matches    12;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db      1 TCATTGAGGCATG 13
          |||| ||||||||
Qy      5 TCATCGAGGCATG 17


RESULT   12
ID   US-08-463-953-37 STANDARD; DNA; UNC; 27 BP.
AC   xxxxxx
DT
DE   Sequence 37, Application US/08463953
CC   Sequence 37, Application US/08463953
CC   Patent No. 5502034
CC    GENERAL INFORMATION:
CC      APPLICANT:  Holly, Richard D.
CC      APPLICANT:  Foster, Donald C.
CC      TITLE OF INVENTION:  METHODS FOR PRODUCING THROMBIN
CC      NUMBER OF SEQUENCES:  48
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Townsend and Townsend
CC        STREET:  One Market Plaza, Stewart Street Tower,
CC        STREET:  Twentieth Floor
CC        CITY:  San Francisco
CC        STATE:  CA
CC        COUNTRY:  USA
CC        ZIP:  94105
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, Version #1.25
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/463,953
CC        FILING DATE:
CC        CLASSIFICATION:  514
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  US 07/860,701
CC        FILING DATE:  31-MAR-1992
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  US 07/816,281
CC        FILING DATE:  31-DEC-1991
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Parmelee, Steven W
CC        REGISTRATION NUMBER:  31,990
CC        REFERENCE/DOCKET NUMBER:  13952-12-2
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  206-467-9600
CC        TELEFAX:  415-543-5043
CC    INFORMATION FOR SEQ ID NO:  37:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  27 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  single
CC        TOPOLOGY:  linear
CC      IMMEDIATE SOURCE:
CC        CLONE:  ZC1551
SQ   SEQUENCE 27 BP; 4 A; 9 C; 10 G; 4 T; 0 OTHER.

  Query Match           61.1%;  Score 11;  DB 1;  Length 27;
  Best Local Similarity  92.3%;  Pred. No. 1.83e+02;
  Matches    12;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db     15 TCCTCGAGGCATG 27
          || ||||||||||
Qy      5 TCATCGAGGCATG 17


RESULT   13
ID   PCT-US93-12687-7 STANDARD; DNA; UNC; 27 BP.
AC   xxxxxx
DT
DE   Sequence 7, Application PC/TUS9312687
CC   Sequence 7, Application PC/TUS9312687
CC    GENERAL INFORMATION:
CC      APPLICANT:  Irani, Meher H.
CC      TITLE OF INVENTION:  HYBRID CROSS-LINKING PROTEINS
CC      NUMBER OF SEQUENCES:  14
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  ZymoGenetics, Inc.
CC        STREET:  4225 Roosevelt Way, N.E.
CC        CITY:  Seattle
CC        STATE:  WA
CC        COUNTRY:  USA
CC        ZIP:  98105
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, Version #1.25
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  PCT/US93/12687
CC        FILING DATE:
CC        CLASSIFICATION:
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  US 07/998,271
```

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CC        FILING DATE:  31-DEC-1992
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Parker, Gary E
CC        REGISTRATION NUMBER:  31-648
CC        REFERENCE/DOCKET NUMBER:  92-26PC
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  206-547-8080 ext 322
CC        TELEFAX:  206-548-2329
CC    INFORMATION FOR SEQ ID NO:  7:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  27 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  single
CC        TOPOLOGY:  linear
CC      IMMEDIATE SOURCE:
CC        CLONE:  ZC1551
SQ   SEQUENCE 27 BP; 4 A; 9 C; 10 G; 4 T; 0 OTHER.

  Query Match           61.1%;  Score 11;  DB 4;  Length 27;
  Best Local Similarity  92.3%;  Pred. No. 1.83e+02;
  Matches   12;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db     15 TCCTCGAGGCATG 27
          || ||||||||||
Qy      5 TCATCGAGGCATG 17


RESULT   14
ID   US-07-998-972A-37 STANDARD; DNA; UNC; 27 BP.
AC   xxxxxx
DT
DE   Sequence 37, Application US/07998972A
CC   Sequence 37, Application US/07998972A
CC   Patent No. 5476777
CC    GENERAL INFORMATION:
CC      APPLICANT:  Holly, Richard D.
CC      APPLICANT:  Foster, Donald C.
CC      TITLE OF INVENTION:  METHODS FOR PRODUCING THROMBIN
CC      NUMBER OF SEQUENCES:  48
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Townsend and Townsend
CC        STREET:  One Market Plaza, Stewart Street Tower,
CC        STREET:  Twentieth Floor
CC        CITY:  San Francisco
CC        STATE:  CA
CC        COUNTRY:  USA
CC        ZIP:  94105
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, Version #1.25
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/07/998,972A
CC        FILING DATE:  19921230
CC        CLASSIFICATION:  435
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  US 07/860,701
CC        FILING DATE:  31-MAR-1992
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  US 07/816,281
CC        FILING DATE:  31-DEC-1991
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Parmelee, Steven W
CC        REGISTRATION NUMBER:  31,990
CC        REFERENCE/DOCKET NUMBER:  13952-12-2
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  206-467-9600
CC        TELEFAX:  415-543-5043
CC    INFORMATION FOR SEQ ID NO:  37:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  27 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  single
CC        TOPOLOGY:  linear
CC      IMMEDIATE SOURCE:
CC        CLONE:  ZC1551
SQ   SEQUENCE 27 BP; 4 A; 9 C; 10 G; 4 T; 0 OTHER.

  Query Match           61.1%;  Score 11;  DB 1;  Length 27;
  Best Local Similarity  92.3%;  Pred. No. 1.83e+02;
  Matches   12;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db     15 TCCTCGAGGCATG 27
          || ||||||||||
Qy      5 TCATCGAGGCATG 17


RESULT   15
ID   US-08-462-261-37 STANDARD; DNA; UNC; 27 BP.
AC   xxxxxx
DT
DE   Sequence 37, Application US/08462261
CC   Sequence 37, Application US/08462261
CC   Patent No. 5527692
CC    GENERAL INFORMATION:
CC      APPLICANT:  Holly, Richard D.
CC      APPLICANT:  Foster, Donald C.
CC      TITLE OF INVENTION:  METHODS FOR PRODUCING THROMBIN
CC      NUMBER OF SEQUENCES:  48
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Townsend and Townsend
CC        STREET:  One Market Plaza, Stewart Street Tower,
CC        STREET:  Twentieth Floor
CC        CITY:  San Francisco
CC        STATE:  CA
CC        COUNTRY:  USA
CC        ZIP:  94105
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, Version #1.25
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/462,261
CC        FILING DATE:  05-JUN-1995
CC        CLASSIFICATION:  424
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  US 07/998,972
CC        FILING DATE:  30-DEC-1992
CC        APPLICATION NUMBER:  US 07/860,701
CC        FILING DATE:  31-MAR-1992
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  US 07/816,281
CC        FILING DATE:  31-DEC-1991
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Parmelee, Steven W
CC        REGISTRATION NUMBER:  31,990
CC        REFERENCE/DOCKET NUMBER:  13952-12-2
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  206-467-9600
CC        TELEFAX:  415-543-5043
CC    INFORMATION FOR SEQ ID NO:  37:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  27 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  single
CC        TOPOLOGY:  linear
CC      IMMEDIATE SOURCE:
CC        CLONE:  ZC1551
SQ   SEQUENCE 27 BP; 4 A; 9 C; 10 G; 4 T; 0 OTHER.

  Query Match           61.1%;  Score 11;  DB 1;  Length 27;
  Best Local Similarity  92.3%;  Pred. No. 1.83e+02;
  Matches   12;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;
```

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Db      15 TCCTCGAGGCATG 27
           || ||||||||||
Qy       5 TCATCGAGGCATG 17


RESULT   16
ID   PCT-US92-11357-37 STANDARD; DNA; UNC; 27 BP.
AC   xxxxxx
DT
DE   Sequence 37, Application PC/TUS9211357
CC   Sequence 37, Application PC/TUS9211357
CC    GENERAL INFORMATION:
CC      APPLICANT:  Holly, Richard D.
CC      APPLICANT:  Foster, Donald C.
CC      TITLE OF INVENTION:  METHODS FOR PRODUCING THROMBIN
CC      NUMBER OF SEQUENCES:  48
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Townsend and Townsend
CC        STREET:  One Market Plaza, Stewart Street Tower,
CC        STREET:  Twentieth Floor
CC        CITY:  San Francisco
CC        STATE:  CA
CC        COUNTRY:  USA
CC        ZIP:  94105
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, Version #1.25
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  PCT/US92/11357
CC        FILING DATE:  19921230
CC        CLASSIFICATION:
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  US 07/860,701
CC        FILING DATE:  31-MAR-1992
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  US 07/816,281
CC        FILING DATE:  31-DEC-1991
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Parmelee, Steven W
CC        REGISTRATION NUMBER:  31,990
CC        REFERENCE/DOCKET NUMBER:  13952-12-2
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  206-467-9600
CC        TELEFAX:  415-543-5043
CC    INFORMATION FOR SEQ ID NO:  37:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  27 base pairs
CC        TYPE:  NUCLEIC ACID
CC        STRANDEDNESS:  single
CC        TOPOLOGY:  linear
CC      IMMEDIATE SOURCE:
CC        CLONE:  ZC1551
SQ   SEQUENCE 27 BP; 4 A; 9 C; 10 G; 4 T; 0 OTHER.

  Query Match           61.1%;  Score 11;  DB 4;  Length 27;
  Best Local Similarity  92.3%;  Pred. No. 1.83e+02;
  Matches    12;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db      15 TCCTCGAGGCATG 27
           || ||||||||||
Qy       5 TCATCGAGGCATG 17


RESULT   17
ID   PCT-US94-07762-2 STANDARD; DNA; UNC; 33 BP.
AC   xxxxxx
DT
DE   Sequence 2, Application PC/TUS9407762
CC   Sequence 2, Application PC/TUS9407762
CC    GENERAL INFORMATION:
CC      APPLICANT:  THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
CC      TITLE OF INVENTION:  GROWTH DIFFERENTIATION FACTOR-6
CC      NUMBER OF SEQUENCES:  21
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Spensley Horn Jubas & Lubitz
CC        STREET:  1880 Century Park East, Suite 500
CC        CITY:  Los Angeles
CC        STATE:  California
CC        COUNTRY:  USA
CC        ZIP:  90067
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, Version #1.25
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  PCT/US94/07762
CC        FILING DATE:  08-JUL-1994
CC        CLASSIFICATION:
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  TUMARKIN, LISA A., PH.D.
CC        REGISTRATION NUMBER:  P-38,347
CC        REFERENCE/DOCKET NUMBER:  FD2349
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  (619) 455-5100
CC        TELEFAX:  (619) 455-5110
CC    INFORMATION FOR SEQ ID NO:  2:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  33 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  single
CC        TOPOLOGY:  linear
CC      MOLECULE TYPE:  DNA (genomic)
CC      IMMEDIATE SOURCE:
CC        CLONE:  SJL145
CC      FEATURE:
CC        NAME/KEY:  CDS
CC        LOCATION:  1..29
CC        OTHER INFORMATION:  /note= "R=adenine or guanine;
CC        OTHER INFORMATION:  S=cytosine or guanine; M=adenine or cytosine;
CC        OTHER INFORMATION:  N=adenine, cytosine, guanine or thymine;
CC        OTHER INFORMATION:  Y=cytosine or thymine; B=inosine"
SQ   SEQUENCE 33 BP; 6 A; 9 C; 3 G; 4 T; 11 OTHER.

  Query Match           61.1%;  Score 11;  DB 4;  Length 33;
  Best Local Similarity  42.9%;  Pred. No. 1.83e+02;
  Matches     6;  Conservative    6;  Mismatches   2;  Indels   0;  Gaps   0;

Db      17 CABGMNTCBACBRY 30
           ||:|: ||:| :::
Cp      17 CATGCCTCGATGAT 4


RESULT   18
ID   US-08-455-559-6 STANDARD; DNA; UNC; 33 BP.
AC   xxxxxx
DT
DE   Sequence 6, Application US/08455559
CC   Sequence 6, Application US/08455559
CC   Patent No. 5801014
CC    GENERAL INFORMATION:
CC      APPLICANT:  LEE, SE-JIN
CC      APPLICANT:  HUYNH, THANH
CC      TITLE OF INVENTION:  GROWTH DIFFERENTIATION FACTOR-5
CC      NUMBER OF SEQUENCES:  27
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  SPENSLEY HORN JUBAS & LUBITZ
CC        STREET:  1880 CENTURY PARK EAST, FIFTH FLOOR
CC        CITY:  LOS ANGELES
CC        STATE:  CALIFORNIA
CC        COUNTRY:  US
CC        ZIP:  90067
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
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CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, Version #1.25
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/455,559
CC         FILING DATE:  31-MAY-1995
CC         CLASSIFICATION:  435
CC       PRIOR APPLICATION DATA:
CC         APPLICATION NUMBER:  US 08/003,144
CC         FILING DATE:  12-JAN-1993
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  WETHERELL, JR. PH.D., JOHN R.
CC         REGISTRATION NUMBER:  31,678
CC         REFERENCE/DOCKET NUMBER:  PD2280
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  619/455-5100
CC         TELEFAX:  619-455-5110
CC     INFORMATION FOR SEQ ID NO:  6:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  33 base pairs
CC         TYPE:  nucleic acid
CC         STRANDEDNESS:  single
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  DNA (genomic)
CC       IMMEDIATE SOURCE:
CC         CLONE:  145
CC       FEATURE:
CC         NAME/KEY:  CDS
CC         LOCATION:  1..33
CC         OTHER INFORMATION:  /note= "WHERE "B" OCCURS, B =
CC         OTHER INFORMATION:  INOSINE"
SQ   SEQUENCE 33 BP; 6 A; 9 C; 3 G; 4 T; 11 OTHER.

  Query Match           61.1%;  Score 11;  DB 3;  Length 33;
  Best Local Similarity  42.9%;  Pred. No. 1.83e+02;
  Matches     6;  Conservative     6;  Mismatches   2;  Indels   0;  Gaps   0;

Db      17 CABGMNTCBACBRY 30
           ||:|: ||:| :::
Cp      17 CATGCCTCGATGAT 4


RESULT   19
ID   PCT-US94-00657-6 STANDARD; DNA; UNC; 33 BP.
AC   xxxxxx
DT
DE   Sequence 6, Application PC/TUS9400657
CC   Sequence 6, Application PC/TUS9400657
CC    GENERAL INFORMATION:
CC      APPLICANT:  SE-JIN LEE
CC      APPLICANT:  HUYNH, THANH
CC      TITLE OF INVENTION:  GROWTH DIFFERENTIATION FACTOR-5
CC      NUMBER OF SEQUENCES:  27
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  SPENSLEY HORN JUBAS & LUBITZ
CC        STREET:  1880 CENTURY PARK EAST, FIFTH FLOOR
CC        CITY:  LOS ANGELES
CC        STATE:  CALIFORNIA
CC        COUNTRY:  US
CC        ZIP:  90067
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, Version #1.25
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  PCT/US94/00657
CC        FILING DATE:  1/12/94
CC        CLASSIFICATION:
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  WETHERELL, JR. PH.D., JOHN R.
CC        REGISTRATION NUMBER:  31,678
CC        REFERENCE/DOCKET NUMBER:  FD3256 CIP OF PD2280
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  619/455-5100
CC        TELEFAX:  619-455-5110
CC    INFORMATION FOR SEQ ID NO:  6:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  33 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  single
CC        TOPOLOGY:  linear
CC      MOLECULE TYPE:  DNA (genomic)
CC      IMMEDIATE SOURCE:
CC        CLONE:  145
CC      FEATURE:
CC        NAME/KEY:  CDS
CC        LOCATION:  1..33
CC        OTHER INFORMATION:  /note= "WHERE "B" OCCURS, B =
CC        OTHER INFORMATION:  INOSINE"
SQ   SEQUENCE 33 BP; 6 A; 9 C; 3 G; 4 T; 11 OTHER.

  Query Match           61.1%;  Score 11;  DB 4;  Length 33;
  Best Local Similarity  42.9%;  Pred. No. 1.83e+02;
  Matches     6;  Conservative     6;  Mismatches   2;  Indels   0;  Gaps   0;

Db      17 CABGMNTCBACBRY 30
           ||:|: ||:| :::
Cp      17 CATGCCTCGATGAT 4


RESULT   20
ID   5164485-3 STANDARD; DNA; UNC; 46 BP.
AC   xxxxxx
DT   01-JAN-1900
DE   Patent No. 5164485.
CC  Patent No. 5164485
CC      APPLICANT: FUJISAWA,YUKIO; ITOH,YASUAKI; NISHIMURA,OSAMU
CC   FUJII,TOMOKO
CC      TITLE OF INVENTION: MODIFIED HEPATITUS B VIRUS SURFACE
CC  ANTIGEN P31 AND PRODUCTION THEREOF
CC      NUMBER OF SEQUENCES: 22
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/07/547,948
CC        FILING DATE: 03-JUL-1990
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER: 898,425
CC        FILING DATE: 20-AUG-1986
CC  SEQ ID NO:3:
CC        LENGTH: 42
SQ   Sequence 46 BP; 8 A; 15 C; 10 G; 9 T; 4 other;

  Query Match           61.1%;  Score 11;  DB 5;  Length 42;
  Best Local Similarity 100.0%;  Pred. No. 1.83e+02;
  Matches    11;  Conservative     0;  Mismatches   0;  Indels   0;  Gaps   0;

Db      19 TCGAGGCATGG 29
           ||||||||||
Qy       8 TCGAGGCATGG 18


RESULT   21
ID   US-08-311-760A-176 STANDARD; DNA; UNC; 15 BP.
AC   xxxxxx
DT
DE   Sequence 176, Application US/08311760A
CC   Sequence 176, Application US/08311760A
CC   Patent No. 5599706
CC    GENERAL INFORMATION:
CC      APPLICANT:  Stinchcomb, Dan T.
CC      APPLICANT:  McSwiggen, James
CC      APPLICANT:  Newton, Roger S.
CC      APPLICANT:  Ramharack, Randy
CC      TITLE OF INVENTION:  RIBOZYME TREATMENT OF DISEASES
CC      TITLE OF INVENTION:  OR CONDITIONS RELATED TO LEVELS OF
CC      TITLE OF INVENTION:  PLASMA LIPOPROTEIN (a) [LP(a)] BY
```

CC TITLE OF INVENTION: INHIBITING APOLIPOPROTEIN
CC TITLE OF INVENTION:
CC NUMBER OF SEQUENCES: 392
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Lyon & Lyon
CC STREET: 633 West Fifth Street
CC STREET: Suite 4700
CC CITY: Los Angeles
CC STATE: California
CC COUNTRY: U.S.A.
CC ZIP: 90071
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
CC MEDIUM TYPE: storage
CC COMPUTER: IBM Compatible
CC OPERATING SYSTEM: IBM P.C. DOS 5.0
CC SOFTWARE: FastSEQ Version 1.5
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/311,760A
CC FILING DATE: September 23, 1994
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER:
CC FILING DATE:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Warburg, Richard
CC REGISTRATION NUMBER: 32,327
CC REFERENCE/DOCKET NUMBER: 208/155
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (213) 489-1600
CC TELEFAX: (213) 955-0440
CC TELEX: 67-3510
CC INFORMATION FOR SEQ ID NO: 176:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 15 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
SQ SEQUENCE 15 BP; 4 A; 3 C; 5 G; 0 T; 3 OTHER.

Query Match 55.6%; Score 10; DB 1; Length 15;
Best Local Similarity 71.4%; Pred. No. 6.87e+02;
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 1 GAGUUAUCGAGGCA 14
|| : |:|||||||
Qy 2 GAATCATCGAGGCA 15

RESULT 22
ID US-08-311-760A-9 STANDARD; DNA; UNC; 15 BP.
AC xxxxxx
DT
DE Sequence 9, Application US/08311760A
CC Sequence 9, Application US/08311760A
CC Patent No. 5599706
CC GENERAL INFORMATION:
CC APPLICANT: Stinchcomb, Dan T.
CC APPLICANT: McSwiggen, James
CC APPLICANT: Newton, Roger S.
CC APPLICANT: Ramharack, Randy
CC TITLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES
CC TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS OF
CC TITLE OF INVENTION: PLASMA LIPOPROTEIN (a) [LP(a)] BY
CC TITLE OF INVENTION: INHIBITING APOLIPOPROTEIN
CC TITLE OF INVENTION:
CC NUMBER OF SEQUENCES: 392
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Lyon & Lyon
CC STREET: 633 West Fifth Street
CC STREET: Suite 4700
CC CITY: Los Angeles
CC STATE: California
CC COUNTRY: U.S.A.
CC ZIP: 90071
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
CC MEDIUM TYPE: storage
CC COMPUTER: IBM Compatible
CC OPERATING SYSTEM: IBM P.C. DOS 5.0
CC SOFTWARE: FastSEQ Version 1.5
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/311,760A
CC FILING DATE: September 23, 1994
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER:
CC FILING DATE:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Warburg, Richard
CC REGISTRATION NUMBER: 32,327
CC REFERENCE/DOCKET NUMBER: 208/155
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (213) 489-1600
CC TELEFAX: (213) 955-0440
CC TELEX: 67-3510
CC INFORMATION FOR SEQ ID NO: 9:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 15 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
SQ SEQUENCE 15 BP; 4 A; 3 C; 5 G; 0 T; 3 OTHER.

Query Match 55.6%; Score 10; DB 1; Length 15;
Best Local Similarity 71.4%; Pred. No. 6.87e+02;
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 1 GAGUUAUCGAGGCA 14
|| : |:|||||||
Qy 2 GAATCATCGAGGCA 15

RESULT 23
ID US-07-855-417A-12 STANDARD; DNA; UNC; 20 BP.
AC xxxxxx
DT
DE Sequence 12, Application US/07855417A
CC Sequence 12, Application US/07855417A
CC Patent No. 5484985
CC GENERAL INFORMATION:
CC APPLICANT: Pereira, Heloise Anne
CC APPLICANT: Spitznagel, John K.
CC TITLE OF INVENTION: Chemotactic, Antibiotic and
CC TITLE OF INVENTION: Lipopolysaccharide-Binding Peptide Fragments of CAP37
CC NUMBER OF SEQUENCES: 29
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Needle & Rosenberg, P.C.
CC STREET: 133 Carnegie Way N.W., Suite 400
CC CITY: Atlanta
CC STATE: Georgia
CC COUNTRY: USA
CC ZIP: 30303
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/855,417A
CC FILING DATE: 18-MAR-1992
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/543,151
CC FILING DATE: 25-JUN-1990
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/375,739
CC FILING DATE: 05-JUL-1989

```
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Severson, Mary L.
CC        REGISTRATION NUMBER:  34,927
CC        REFERENCE/DOCKET NUMBER:  0510.024
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  (404) 688-0770
CC        TELEFAX:  (404) 688-9880
CC    INFORMATION FOR SEQ ID NO:  12:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  20 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  single
CC        TOPOLOGY:  linear
CC      MOLECULE TYPE:  DNA (genomic)
SQ   SEQUENCE 20 BP; 1 A; 5 C; 3 G; 6 T; 5 OTHER.

  Query Match           55.6%;  Score 10;  DB 1;  Length 20;
  Best Local Similarity  64.3%;  Pred. No. 6.87e+02;
  Matches     9;  Conservative    3;  Mismatches   2;  Indels   0;  Gaps   0;

Db      2 UGCCTCCYTGRTTY 15
          :|||||  ||:||:
Cp     15 TGCCTCGATGATTC 2


RESULT   24
ID   US-07-969-931-12 STANDARD; DNA; UNC; 20 BP.
AC   xxxxxx
DT
DE   Sequence 12, Application US/07969931
CC   Sequence 12, Application US/07969931
CC   Patent No. 5458874
CC    GENERAL INFORMATION:
CC      APPLICANT:  Pereira, Heloise Anne
CC      APPLICANT:  Spitznagel, John K.
CC      TITLE OF INVENTION:  Chemotactic, Antibiotic and
CC      TITLE OF INVENTION:  Lipopolysaccharide-Binding Peptide Fragments of CAP37
CC      NUMBER OF SEQUENCES:  29
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Needle & Rosenberg, P.C.
CC        STREET:  133 Carnegie Way N.W., Suite 400
CC        CITY:  Atlanta
CC        STATE:  Georgia
CC        COUNTRY:  USA
CC        ZIP:  30303
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, Version #1.25
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/07/969,931
CC        FILING DATE:  19921030
CC        CLASSIFICATION:  514
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  US 07/543,151
CC        FILING DATE:  25-JUN-1990
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  US 07/375,739
CC        FILING DATE:  05-JUL-1989
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Severson, Mary L.
CC        REGISTRATION NUMBER:  34,927
CC        REFERENCE/DOCKET NUMBER:  0510.024
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  (404) 688-0770
CC        TELEFAX:  (404) 688-9880
CC    INFORMATION FOR SEQ ID NO:  12:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  20 base pairs
CC        TYPE:  NUCLEIC ACID
CC        STRANDEDNESS:  single
CC        TOPOLOGY:  linear
CC      MOLECULE TYPE:  DNA (genomic)
SQ   SEQUENCE 20 BP; 1 A; 5 C; 3 G; 6 T; 5 OTHER.

  Query Match           55.6%;  Score 10;  DB 1;  Length 20;
  Best Local Similarity  64.3%;  Pred. No. 6.87e+02;
  Matches     9;  Conservative    3;  Mismatches   2;  Indels   0;  Gaps   0;

Db      2 UGCCTCCYTGRTTY 15
          :|||||  ||:||:
Cp     15 TGCCTCGATGATTC 2


RESULT   25
ID   PCT-US96-09455A-61 STANDARD; DNA; UNC; 21 BP.
AC   xxxxxx
DT
DE   Sequence 61, Application PC/TUS9609455A
CC   Sequence 61, Application PC/TUS9609455A
CC    GENERAL INFORMATION:
CC      APPLICANT:  PARMA, et al.
CC      TITLE OF INVENTION:  HIGH AFFINITY NUCLEIC ACID
CC      TITLE OF INVENTION:  LIGANDS TO LECTINS
CC      NUMBER OF SEQUENCES:  390
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Swanson & Bratschun, L.L.C.
CC        STREET:  8400 E. Prentice Avenue, Suite 200
CC        CITY:  Englewood
CC        STATE:  Colorado
CC        COUNTRY:  USA
CC        ZIP:  80111
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Diskette, 3 1/2 diskette, 1.44 MB
CC        COMPUTER:  IBM pc compatible
CC        OPERATING SYSTEM:  MS-DOS
CC        SOFTWARE:  WordPerfect 6.0
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  PCT/US96/09455A
CC        FILING DATE:  05 JUNE 1996
CC        CLASSIFICATION:
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  08/479,724
CC        FILING DATE:  07-JUNE-1995
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  08/472,256
CC        FILING DATE:  07-JUNE-1995
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  08/472,255
CC        FILING DATE:  07-JUNE-1995
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  08/477,829
CC        FILING DATE:  07-JUNE-1995
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Barry J. Swanson
CC        REGISTRATION NUMBER:  33,215
CC        REFERENCE/DOCKET NUMBER:  NEX40C/PCT
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  (303) 793-3333
CC        TELEFAX:  (303) 793-3433
CC    INFORMATION FOR SEQ ID NO:  61:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  21 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  single
CC        TOPOLOGY:  linear
CC      MOLECULE TYPE:  RNA
CC      FEATURE:
CC        OTHER INFORMATION:  All C's are 2'-NH2 cytosine
CC      FEATURE:
CC        OTHER INFORMATION:  All U's are 2'-NH2 uracil
SQ   SEQUENCE 21 BP; 2 A; 3 C; 8 G; 0 T; 8 OTHER.

  Query Match           55.6%;  Score 10;  DB 4;  Length 21;
  Best Local Similarity  50.0%;  Pred. No. 6.87e+02;
```

```
  Matches    7;  Conservative    5;  Mismatches   2;  Indels   0;  Gaps   0;

Db       8 UGACYCGRGGAYUC 21
           :| |:||: ||::|
Cp      15 TGCCTCGATGATTC 2


RESULT   26
ID   US-08-479-724A-61 STANDARD; DNA; UNC; 21 BP.
AC   xxxxxx
DT
DE   Sequence 61, Application US/08479724A
CC   Sequence 61, Application US/08479724A
CC   Patent No. 5780228
CC    GENERAL INFORMATION:
CC      APPLICANT:  PARMA, DAVID
CC      APPLICANT:  GOLD, LARRY
CC      TITLE OF INVENTION:  HIGH AFFINITY NUCLEIC ACID LIGANDS
CC      TITLE OF INVENTION:  TO LECTINS
CC      NUMBER OF SEQUENCES:  173
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Swanson & Bratschun, L.L.C.
CC        STREET:  8400 E. Prentice Avenue, Suite 200
CC        CITY:  Englewood
CC        STATE:  Colorado
CC        COUNTRY:  USA
CC        ZIP:  80111
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Diskette, 3 1/2 diskette, 1.44 MB
CC        COMPUTER:  IBM pc compatible
CC        OPERATING SYSTEM:  MS-DOS
CC        SOFTWARE:  WordPerfect 6.0
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/479,724A
CC        FILING DATE:  07-JUNE-1995
CC        CLASSIFICATION:  435
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  07/714,131
CC        FILING DATE:  10-JUNE-1991
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  07/536,428
CC        FILING DATE:  11-JUNE-1991
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  07/964,624
CC        FILING DATE:  21-OCTOBER-1992
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Barry J. Swanson
CC        REGISTRATION NUMBER:  33,215
CC        REFERENCE/DOCKET NUMBER:  NEX40-1
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  (303) 793-3333
CC        TELEFAX:  (303) 793-3433
CC     INFORMATION FOR SEQ ID NO:  61:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  21 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  single
CC        TOPOLOGY:  linear
CC      MOLECULE TYPE:  RNA
CC      FEATURE:
CC        OTHER INFORMATION:  All C's are 2'-NH2 cytosine
CC      FEATURE:
CC        OTHER INFORMATION:  All U's are 2'-NH2 uracil
SQ   SEQUENCE 21 BP; 2 A; 3 C; 8 G; 0 T; 8 OTHER.

  Query Match           55.6%;  Score 10;  DB 3;  Length 21;
  Best Local Similarity  50.0%;  Pred. No. 6.87e+02;
  Matches    7;  Conservative    5;  Mismatches   2;  Indels   0;  Gaps   0;

Db       8 UGACYCGRGGAYUC 21
           :| |:||: ||::|
Cp      15 TGCCTCGATGATTC 2


RESULT   27
ID   US-08-181-556-11 STANDARD; DNA; UNC; 23 BP.
AC   xxxxxx
DT
DE   Sequence 11, Application US/08181556
CC   Sequence 11, Application US/08181556
CC   Patent No. 5525486
CC    GENERAL INFORMATION:
CC      APPLICANT:  HONJO, Tasuku
CC      APPLICANT:  TASHIRO, Kei
CC      APPLICANT:  TADA, Hideaki
CC      TITLE OF INVENTION:  PROCESS FOR CONSTRUCTING cDNA LIBRARY,
CC      TITLE OF INVENTION:  AND NOVEL POLYPEPTIDE AND DNA CODING FOR THE SAME
CC      NUMBER OF SEQUENCES:  11
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  STEVENS, DAVIS, MILLER & MOSHER
CC        STREET:  515 No. 5525486th Washington Street (P.O. Box 1427)
CC        CITY:  Alexandria
CC        STATE:  Virginia
CC        COUNTRY:  USA
CC        ZIP:  22313
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, Version #1.25
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/181,556
CC        FILING DATE:  14-JAN-1994
CC        CLASSIFICATION:  424
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  JP 5-22098
CC        FILING DATE:  14-JAN-1993
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  POULOS III, James A.
CC        REGISTRATION NUMBER:  31714
CC        REFERENCE/DOCKET NUMBER:  TPP/29088
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  (703) 549-7200
CC        TELEFAX:  (703) 528-5313
CC        TELEX:  89-2746
CC     INFORMATION FOR SEQ ID NO:  11:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  23 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  single
CC        TOPOLOGY:  linear
CC      MOLECULE TYPE:  cDNA to mRNA
CC      FEATURE:
CC        NAME/KEY:  modified_base
CC        LOCATION:  1..23
CC        OTHER INFORMATION:  /note= "A 17 mer dA ligated to a
CC        OTHER INFORMATION:  restriction enzyme site containing EcoRI (the 3'
CC        OTHER INFORMATION:  end)."
SQ   SEQUENCE 23 BP; 4 A; 8 C; 8 G; 3 T; 0 OTHER.

  Query Match           55.6%;  Score 10;  DB 1;  Length 23;
  Best Local Similarity  85.7%;  Pred. No. 6.87e+02;
  Matches    12;  Conservative    0;  Mismatches   2;  Indels   0;  Gaps   0;

Db      10 GCCTCGAGGAATCC 23
           ||||||| || |||
Cp      14 GCCTCGATGATTCC 1


RESULT   28
ID   US-08-474-633A-19 STANDARD; DNA; UNC; 27 BP.
AC   xxxxxx
DT
DE   Sequence 19, Application US/08474633A
CC   Sequence 19, Application US/08474633A
CC   Patent No. 5773691
```

```
CC    GENERAL INFORMATION:
CC      APPLICANT:  E. I. DU PONT DE NEMOURS AND
CC      APPLICANT:  COMPANY
CC      TITLE OF INVENTION:  CHIMERIC GENES AND
CC      TITLE OF INVENTION:  METHODS FOR INCREASING
CC      TITLE OF INVENTION:  INCREASING THE LYSINE
CC      TITLE OF INVENTION:  AND THREONINE CONTENT
CC      TITLE OF INVENTION:  OF THE SEEDS OF PLANTS
CC      NUMBER OF SEQUENCES:  107
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  E. I. DU PONT DE NEMOURS
CC        ADDRESSEE:  AND COMPANY
CC        STREET:  1007 MARKET STREET
CC        CITY:  WILMINGTON
CC        STATE:  DELAWARE
CC        COUNTRY:  U.S.A.
CC        ZIP:  19898
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  FLOPPY DISK
CC        COMPUTER:  IBM PC COMPATIBLE
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  MICROSOFT WORD VERSION 2.0C
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/474,633A
CC        FILING DATE:
CC        CLASSIFICATION:  800
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  BARBARA C. SIEGELL
CC        REGISTRATION NUMBER:  30,684
CC        REFERENCE/DOCKET NUMBER:  BB-1037-C
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  302-992-4931
CC        TELEFAX:  302-773-0164
CC        TELEX:  835420
CC    INFORMATION FOR SEQ ID NO:  19:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  27 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  single
CC        TOPOLOGY:  linear
CC      MOLECULE TYPE:  DNA (genomic)
CC      FEATURE:
CC        NAME/KEY:  misc_feature
CC        LOCATION:  1..27
CC        OTHER INFORMATION:  /product= "synthetic
CC        OTHER INFORMATION:  oligonucleotide"
CC        OTHER INFORMATION:  /standard_name= "SM
CC        OTHER INFORMATION:  79"
SQ    SEQUENCE 27 BP; 6 A; 8 C; 8 G; 5 T; 0 OTHER.

  Query Match           55.6%;  Score 10;  DB 3;  Length 27;
  Best Local Similarity  81.3%;  Pred. No. 6.87e+02;
  Matches    13;  Conservative    0;  Mismatches   3;  Indels   0;  Gaps   0;

Db       8 ATGCCACGATGCGTCC 23
           ||||| |||||  |||
Cp      16 ATGCCTCGATGATTCC 1


RESULT   29
ID    US-08-182-175A-12 STANDARD; DNA; UNC; 27 BP.
AC    xxxxxx
DT
DE    Sequence 12, Application US/08182175A
CC    Sequence 12, Application US/08182175A
CC    Patent No. 5559223
CC     GENERAL INFORMATION:
CC       APPLICANT:  Saverio Carl Falco
CC       APPLICANT:  Sharon J. Keeler
CC       APPLICANT:  Janet A. Rice
CC       TITLE OF INVENTION:  Synthetic Storage Proteins with Defined Structure Containin
CC       NUMBER OF SEQUENCES:  113
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  E.I. du Pont de Nemours and Company
CC         STREET:  1007 Market Street
CC         CITY:  Wilmington
CC         STATE:  Delaware
CC         COUNTRY:  USA
CC         ZIP:  19898
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy Disk
CC         COMPUTER:  Macintosh
CC         OPERATING SYSTEM:  Macintosh System, 6.0
CC         SOFTWARE:  Microsoft Word, 4.0
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/182,175A
CC         FILING DATE:
CC         CLASSIFICATION:  800
CC       PRIOR APPLICATION DATA:
CC         APPLICATION NUMBER:  07/743,006
CC         FILING DATE:  9 August 1991
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Linda Axamethy Floyd
CC         REGISTRATION NUMBER:  33,692
CC         REFERENCE/DOCKET NUMBER:  BB-1031
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  (302) 992-4929
CC         TELEFAX:  (302) 892-7949
CC         TELEX:  835420
CC     INFORMATION FOR SEQ ID NO:  12:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  27 base pairs
CC         TYPE:  nucleic acid
CC         STRANDEDNESS:  single
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  DNA (genomic)
CC       FEATURE:
CC         NAME/KEY:  misc_feature
CC         LOCATION:  1..27
CC         OTHER INFORMATION:  /product= "synthetic oligonucleotide"
CC         OTHER INFORMATION:  /standard_name= "SM 79"
SQ    SEQUENCE 27 BP; 6 A; 8 C; 8 G; 5 T; 0 OTHER.

  Query Match           55.6%;  Score 10;  DB 1;  Length 27;
  Best Local Similarity  81.3%;  Pred. No. 6.87e+02;
  Matches    13;  Conservative    0;  Mismatches   3;  Indels   0;  Gaps   0;

Db       8 ATGCCACGATGCGTCC 23
           ||||| |||||  |||
Cp      16 ATGCCTCGATGATTCC 1


RESULT   30
ID    PCT-US92-06412-12 STANDARD; DNA; UNC; 27 BP.
AC    xxxxxx
DT
DE    Sequence 12, Application PC/TUS9206412
CC    Sequence 12, Application PC/TUS9206412
CC     GENERAL INFORMATION:
CC       APPLICANT:  Saverio Carl Falco
CC       APPLICANT:  Sharon J. Keeler
CC       APPLICANT:  Janet A. Rice
CC       TITLE OF INVENTION:  Synthetic Storage Proteins with Defined Structure Contai
CC       NUMBER OF SEQUENCES:  113
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  E.I. du Pont de Nemours and Company
CC         STREET:  1007 Market Street
CC         CITY:  Wilmington
CC         STATE:  Delaware
CC         COUNTRY:  USA
CC         ZIP:  19898
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy Disk
CC         COMPUTER:  Macintosh
CC         OPERATING SYSTEM:  Macintosh System, 6.0
CC         SOFTWARE:  Microsoft Word, 4.0
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CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  PCT/US92/06412
CC        FILING DATE:  19920807
CC        CLASSIFICATION:  530
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  07/743,006
CC        FILING DATE:  9 August 1991
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Linda Axamethy Floyd
CC        REGISTRATION NUMBER:  33,692
CC        REFERENCE/DOCKET NUMBER:  BB-1031
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  (302) 992-4929
CC        TELEFAX:  (302) 892-7949
CC        TELEX:  835420
CC    INFORMATION FOR SEQ ID NO:  12:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  27 base pairs
CC        TYPE:  NUCLEIC ACID
CC        STRANDEDNESS:  single
CC        TOPOLOGY:  linear
CC      MOLECULE TYPE:  DNA (genomic)
CC      FEATURE:
CC        NAME/KEY:  misc_feature
CC        LOCATION:  1..27
CC        OTHER INFORMATION:  /product= "synthetic oligonucleotide"
CC        OTHER INFORMATION:  /standard_name= "SM 79"
SQ   SEQUENCE 27 BP; 6 A; 8 C; 8 G; 5 T; 0 OTHER.

  Query Match           55.6%;  Score 10;  DB 4;  Length 27;
  Best Local Similarity  81.3%;  Pred. No. 6.87e+02;
  Matches    13;  Conservative    0;  Mismatches   3;  Indels   0;  Gaps   0;

Db       8 ATGCCACGATGCGTCC 23
           ||||| |||||   |||
Cp      16 ATGCCTCGATGATTCC 1

Search completed: Mon Aug  2 12:14:52 1999
Job time : 82 secs.
```

****

MPSRCH (TM)

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MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Mon Aug 2 12:09:45 1999; MasPar time 135.39 Seconds
311.525 Million cell updates/sec

Tabular output not generated.

Title: >US-09-121-239-26
Description: (1-18) from US09121239.seq
Perfect Score: 18
N.A. Sequence: 1 GGAATCATCGAGGCATGG 18
Comp: CCTTAGTAGCTCCGTACC

Scoring table: TABLE default
Gap 10

Nmatch STD : Dbase 0; Query 0

Searched: 2883791 seqs, 1171580779 bases x 2

Post-processing: Minimum Match 0%
Listing first 1000 summaries
Maximum DB seq length 50

Database: embl-est58
1:em_est10 2:em_est11 3:em_est17 4:em_est18 5:em_est2
6:em_est9 7:em_gss1
Database: genbank-est111
8:gb_est1 9:gb_est10 10:gb_est11 11:gb_est12 12:gb_est13
13:gb_est14 14:gb_est15 15:gb_est16 16:gb_est17
17:gb_est18 18:gb_est19 19:gb_est2 20:gb_est20
21:gb_est21 22:gb_est22 23:gb_est23 24:gb_est24
25:gb_est25 26:gb_est26 27:gb_est27 28:gb_est28
29:gb_est29 30:gb_est3 31:gb_est4 32:gb_est5 33:gb_est6
34:gb_est7 35:gb_est8 36:gb_est9 37:gb_gss1 38:gb_gss2
39:gb_gss3 40:gb_gss4 41:gb_gss5 42:gb_gss6

Statistics: Mean 6.252; Variance 1.127; scale 5.546

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.

No matches found.

Search completed: Mon Aug 2 12:14:48 1999
Job time : 303 secs.

****

MPSRCH (TM)

****

Release 3.1A John F. Collins, Biocomputing Research Unit.

MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Mon Aug 2 12:19:42 1999; MasPar time 133.50 Seconds
539.865 Million cell updates/sec

Tabular output not generated.

Title: >US-09-121-239-27
Description: (1-26) from US09121239.seq
Perfect Score: 26
N.A. Sequence: 1 CACTCAGCCACTGGATTTAAGCAGAG 26
Comp: GTGAGTCGGTGACCTAAATTCGTCTC

Scoring table: TABLE default
Gap 10

Nmatch STD : Dbase 0; Query 0

Searched: 646147 seqs, 1385953633 bases x 2

Post-processing: Minimum Match 0%
Listing first 1000 summaries
Maximum DB seq length 50

Database: embl58
1:em_ba1 2:em_ba2 3:em_fun 4:em_htg 5:em_hum1 6:em_hum2
7:em_in 8:em_om 9:em_or 10:em_ov 11:em_pat 12:em_ph
13:em_pl 14:em_ro 15:em_sts 16:em_vi
Database: genbank111
17:gb_ba1 18:gb_ba2 19:gb_htg1 20:gb_htg2 21:gb_in1
22:gb_in2 23:gb_om 24:gb_ov 25:gb_pat 26:gb_ph 27:gb_pl1
28:gb_pl2 29:gb_pr1 30:gb_pr2 31:gb_pr3 32:gb_ro
33:gb_st 34:gb_sts 35:gb_sy 36:gb_un 37:gb_vi

Statistics: Mean 7.011; Variance 3.159; scale 2.219

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.

No matches found.

Search completed: Mon Aug 2 12:26:05 1999
Job time : 383 secs.

****

MPSRCH (TM)

****

MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Mon Aug 2 12:32:12 1999; MasPar time 33.71 Seconds
165.278 Million cell updates/sec

Tabular output not generated.

Title: >US-09-121-239-27
Description: (1-26) from US09121239.seq
Perfect Score: 26
N.A. Sequence: 1 CACTCAGCCACTGGATTTAAGCAGAG 26
Comp: GTGAGTCGGTGACCTAAATTCGTCTC

Scoring table: TABLE default
Gap 10

Nmatch STD : Dbase 0; Query 0

Searched: 271905 seqs, 107135622 bases x 2

Post-processing: Minimum Match 0%
Listing first 1000 summaries
Maximum DB seq length 50

Database: n-geneseq35
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33
34:part34 35:part35 36:part36 37:part37 38:part38
39:part39 40:part40 41:part41 42:part42 43:part43
44:part44 45:part45 46:part46 47:part47 48:part48
49:part49 50:part50 51:part51 52:part52 53:part53
54:part54 55:part55 56:part56 57:part57 58:part58
59:part59 60:part60

Statistics: Mean 5.552; Variance 3.164; scale 1.755

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description	Pred. No.
1		21	80.8	40	45	V39474	Chronic myelogenous l	1.70e-02
c 2		18	69.2	18	45	V39476	Chronic myelogenous l	8.95e-01
c 3		18	69.2	18	3	Q21921	3'-tandem oligomer to	8.95e-01
4		16	61.5	39	6	Q37185	Ribozyme gene insert	1.12e+01
c 5		15	57.7	40	10	Q57149	Chromosomal transloca	3.77e+01
c 6		14	53.8	18	45	V39477	Chronic myelogenous l	1.23e+02
7		14	53.8	30	6	Q37186	Bcr-abl mRMA sequence	1.23e+02
c 8		14	53.8	31	40	V01787	Antisense RNA sequenc	1.23e+02
c 9		13	50.0	17	1	N81469	Probe to B-cell diffe	3.86e+02
c 10		13	50.0	17	10	Q56274	Sequence of Probe No.	3.86e+02
11		13	50.0	18	9	Q51833	bcr mRNA ribozyme cle	3.86e+02
12		13	50.0	22	6	Q34636	Human bcr exon 3 5' P	3.86e+02
c 13		13	50.0	30	40	V01786	Antisense RNA sequenc	3.86e+02
c 14		13	50.0	40	40	V01804	Antisense RNA sequenc	3.86e+02
c 15		12	46.2	17	59	V97763	Human EGF-R target se	1.16e+03
16		12	46.2	18	3	Q14330	MCPC 603 VL CDR1 walk	1.16e+03
c 17		12	46.2	21	5	Q28817	HLA Class II gene loc	1.16e+03
18		12	46.2	28	12	Q74572	Probe for the detecti	1.16e+03
c 19		12	46.2	28	12	Q74497	Probe for the detecti	1.16e+03
c 20		12	46.2	28	15	Q86609	Human immunodeficienc	1.16e+03
c 21		12	46.2	29	56	V92356	Human A-Raf hammerhea	1.16e+03
c 22		12	46.2	33	7	Q46735	HIV amplifier probe H	1.16e+03
c 23		12	46.2	33	15	Q89511	Human immunodeficienc	1.16e+03
24		12	46.2	34	15	Q86488	Primer, e24, for ampl	1.16e+03
25		12	46.2	36	4	Q25115	PCR primer 21/M6.	1.16e+03
26		12	46.2	36	4	Q25114	PCR primer 21/M5.	1.16e+03
27		12	46.2	39	2	Q11446	Probe #8 complementar	1.16e+03
28		12	46.2	39	2	Q11451	Probe #13 complementa	1.16e+03
29		12	46.2	46	8	Q49401	HIV-1 TATA region.	1.16e+03
30		12	46.2	49	37	T95880	Competitor of 43 kDa	1.16e+03
31		12	46.2	50	25	T64198	Human T-cell lymphotr	1.16e+03
32		12	46.2	50	11	Q69737	AIDS-associated retro	1.16e+03
33		12	46.2	50	11	Q69736	Human T-cell lymphotr	1.16e+03
34		12	46.2	50	50	V65660	HIV-1 TATA region oli	1.16e+03

Note: Post-processor removed 964 summaries from list due to search parameters chosen.

ALIGNMENTS

RESULT 1
ID V39474 standard; DNA; 40 BP.
AC V39474;
DT 22-SEP-1998 (first entry)
DE Chronic myelogenous leukaemia model target oligonucleotide.
KW Acute lymphocytic leukaemia; Chronic myelogenous leukaemia; ALL; CML;
KW target; capture probe; detection probe; hybridisation; bcr; abl;
KW multiple analyte; Salmonella; chromasomal translocation;
KW Philadelphia chromosome; ss.
OS Synthetic.
OS Homo sapiens.
PN EP-846776-A2.
PD 10-JUN-1998.
PF 05-DEC-1997; 309831.
PR 06-DEC-1996; US-761131.
PA (VYSI-) VYSIS INC.
PI Lane DJ, Muller UR;
DR WPI; 98-299988/27.
PT Assay device for isolating analyte from sample, e.g. Salmonella in
PT food - comprises tube containing linear array of binding elements,
PT linked to binding factor to which component binds
PS Example 2; Page 12; 25pp; English.
CC An assay device has been developed for isolating an analyte from a
CC sample. The assay device comprises a tube containing a linear array of
CC binding elements, each linked to a distinct binding factor to which a
CC corresponding specific component binds, where each of the binding
CC elements is configured to sealingly contact the interior surface of the
CC tube along the entire circumference of the binding element. The present
CC sequence represents a model target used in an example from the present
CC invention for the detection of chromosomal translocations. The new
CC method and device can be used to detect e.g. Salmonella in a food
CC sample. They are also used to detect chromasomal translocations to
CC detect the 'Philadelphia' chromosome responsible for acute lymphocytic
CC leukaemia and chronic myelogenous leukaemia.
SQ Sequence 40 BP; 10 A; 10 C; 8 G; 12 T;

Query Match 80.8%; Score 21; DB 45; Length 40;
Best Local Similarity 95.7%; Pred. No. 1.70e-02;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 actcagccactggatttaagtag 23

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                    ||||||||||||||||||||  ||
Qy       2 ACTCAGCCACTGGATTTAAGCAG 24


RESULT    2
ID   V39476 standard; DNA; 18 BP.
AC   V39476;
DT   22-SEP-1998  (first entry)
DE   Chronic myelogenous leukaemia capture probe.
KW   Acute lymphocytic leukaemia; Chronic myelogenous leukaemia; ALL; CML;
KW   target; capture probe; detection probe; hybridisation; bcr; abl;
KW   multiple analyte; Salmonella; chromasomal translocation;
KW   Philadelphia chromosome; ss.
OS   Synthetic.
OS   Homo sapiens.
PN   EP-846776-A2.
PD   10-JUN-1998.
PF   05-DEC-1997; 309831.
PR   06-DEC-1996; US-761131.
PA   (VYSI-) VYSIS INC.
PI   Lane DJ, Muller UR;
DR   WPI; 98-299988/27.
PT   Assay device for isolating analyte from sample, e.g. Salmonella in
PT   food - comprises tube containing linear array of binding elements,
PT   linked to binding factor to which component binds
PS   Example 2; Page 12; 25pp; English.
CC   An assay device has been developed for isolating an analyte from a
CC   sample. The assay device comprises a tube containing a linear array of
CC   binding elements, each linked to a distinct binding factor to which a
CC   corresponding specific component binds, where each of the binding
CC   elements is configured to sealingly contact the interior surface of the
CC   tube along the entire circumference of the binding element. The present
CC   sequence represents a capture probe used in an example from the present
CC   invention for the detection of chromosomal translocations. The new
CC   method and device can be used to detect e.g. Salmonella in a food
CC   sample. They are also used to detect chromasomal translocations to
CC   detect the 'Philadelphia' chromosome responsible for acute lymphocytic
CC   leukaemia and chronic myelogenous leukaemia.
SQ   Sequence   18 BP;    5 A;    3 C;    5 G;    5 T;

  Query Match           69.2%;  Score 18;  DB 45;  Length 18;
  Best Local Similarity 100.0%;  Pred. No. 8.95e-01;
  Matches   18;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db       1 taaatccagtggctgagt 18
           ||||||||||||||||||
Cp      19 TAAATCCAGTGGCTGAGT 2


RESULT    3
ID   Q21921 standard; DNA; 18 BP.
AC   Q21921;
DT   25-JUN-1992  (first entry)
DE   3'-tandem oligomer to disrupt bcr/abl junction secondary structure.
KW   Philadelphia chromosome; CML; P210(abl/bcr) protein expression;
KW   antisense therapy; methylphosphonate oligonucleotide; ss.
OS   Synthetic.
FH   Key             Location/Qualifiers
FT   misc_feature    2..3
FT                   /*tag=  a
FT                   /label= non-phosphodiester_bond
FT                   /note= "see comments"
FT   misc_feature    3..4
FT                   /*tag=  b
FT                   /label= non-phosphodiester_bond
FT                   /note= "see comments"
FT   misc_feature    4..5
FT                   /*tag=  c
FT                   /label= non-phosphodiester_bond
FT                   /note= "see comments"
FT   misc_feature    5..6
FT                   /*tag=  d
FT                   /label= non-phosphodiester_bond
FT                   /note= "see comments"
FT   misc_feature    6..7
FT                   /*tag=  e
FT                   /label= non-phosphodiester_bond
FT                   /note= "see comments"
FT   misc_feature    7..8
FT                   /*tag=  f
FT                   /label= non-phosphodiester_bond
FT                   /note= "see comments"
FT   misc_feature    8..9
FT                   /*tag=  g
FT                   /label= non-phosphodiester_bond
FT                   /note= "see comments"
FT   misc_feature    9..10
FT                   /*tag=  h
FT                   /label= non-phosphodiester_bond
FT                   /note= "see comments"
FT   misc_feature    10..11
FT                   /*tag=  i
FT                   /label= non-phosphodiester_bond
FT                   /note= "see comments"
FT   misc_feature    11..12
FT                   /*tag=  j
FT                   /label= non-phosphodiester_bond
FT                   /note= "see comments"
FT   misc_feature    12..13
FT                   /*tag=  k
FT                   /label= non-phosphodiester_bond
FT                   /note= "see comments"
FT   misc_feature    13..14
FT                   /*tag=  l
FT                   /label= non-phosphodiester_bond
FT                   /note= "see comments"
FT   misc_feature    14..15
FT                   /*tag=  m
FT                   /label= non-phosphodiester_bond
FT                   /note= "see comments"
FT   misc_feature    15..16
FT                   /*tag=  n
FT                   /label= non-phosphodiester_bond
FT                   /note= "see comments"
FT   misc_feature    16..17
FT                   /*tag=  o
FT                   /label= non-phosphodiester_bond
FT                   /note= "see comments"
FT   misc_feature    17..18
FT                   /*tag=  p
FT                   /label= non-phosphodiester_bond
FT                   /note= "see comments"
PN   WO9202641-A.
PD   20-FEB-1992.
PF   09-AUG-1991; 105690.
PR   09-AUG-1990; US-565299.
PA   (GENT-) GENTA INC.
PI   Vaghefi MM, Reynolds MA, Arnold LJ;
DR   WPI; 92-080093/10.
PT   Reagents for conjugating psoralen(s) to oligo-nucleotide(s) -
PT   useful for down regulation of tyrosine kinase activity in
PT   treatment of chronic myelogenous leukaemia
PS   Example 15; Page 32; 67pp; English.
CC   This sequence was used with a 5'-tandem oligomer (see Q21920) to
CC   disrupt the secondary structure of the bcr/abl junction. Both
CC   methylphosphonate oligomers were prepared with a single
CC   phosphodiester linkage at the 5'-end to improve their water
CC   solubility. See also Q21919.
SQ   Sequence   18 BP;    5 A;    3 C;    6 G;    4 T;

  Query Match           69.2%;  Score 18;  DB 3;  Length 18;
  Best Local Similarity 100.0%;  Pred. No. 8.95e-01;
  Matches   18;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db       1 aaatccagtggctgagtg 18
           ||||||||||||||||||
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Cp     18 AAATCCAGTGGCTGAGTG 1


RESULT    4
ID   Q37185 standard; DNA; 39 BP.
AC   Q37185;
DT   13-NOV-1992  (first entry)
DE   Ribozyme gene insert oligonucleotide (2).
KW   Hammerhead; ribozyme; bcr-abl; catalytic domain; target; ss.
OS   Synthetic.
PN   WO9303141-A.
PD   18-FEB-1993.
PF   01-AUG-1991; U05443.
PR   01-AUG-1991; WO-U05443.
PA   (CITY ) CITY OF HOPE.
PI   Forman SJ,  Rossi JJ,  Snyder DS;
DR   WPI; 93-076498/09.
PT   Purging leukaemia cells from bone marrow - by ex vivo treatment
PT   with a ribozyme that inhibits expression of BCR-ABL gene prod.
PS   Disclosure; Page 9; 30pp; English.
CC   A "hammerhead" ribozyme to cleave bcr-abl mRNA was prepd.  The
CC   ribozyme contains a 22 nucleotide catalytic RNA sequence flanked by 15
CC   nucleotide targeting sequences that position the catalytic domain at
CC   the target site by Watson-Crick base pairing.
CC   The double-stranded ribozyme gene insert with two flanking BamHI
CC   restriction sites were prepd. from two single-stranded
CC   oligonucleotides (Q37184-85).
SQ   Sequence   39 BP;    9 A;    10 C;    9 G;    11 T;

  Query Match           61.5%;  Score 16;  DB 6;  Length 39;
  Best Local Similarity 100.0%;  Pred. No. 1.12e+01;
  Matches   16;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db      7 ctggatttaagcagag 22
          ||||||||||||||||
Qy     11 CTGGATTTAAGCAGAG 26


RESULT    5
ID   Q57149 standard; DNA; 40 BP.
AC   Q57149;
DT   26-JUL-1994  (first entry)
DE   Chromosomal translocation detection probe #58.
KW   Probe; detection; chromosomal translocation; leukemia; sarcoma;
KW   lymphoma; chondrodysplasia; Praeder-Willi syndrome; trisomy;
KW   endocrine dysplasia; muscular hypotonia; incontinentia pigmenti;
KW   rhabdo-myosarcoma; myelodysplasia; refractory anaemia;
KW   balanced X-autosome; Beckwith-Weidermann syndrome; ss.
OS   Synthetic.
PN   WO9402500-A.
PD   03-FEB-1994.
PF   16-JUL-1993; U06674.
PR   17-JUL-1992; US-915900.
PA   (APRO-) APROGENEX INC.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Asgari M,  Blick M,  Bresser J,  Cubbage ML,  Ju SC;
PI   Prashad N, Reading CL,  Weber WD;
DR   WPI; 94-048785/06.
PT   Oligonucleotides for detecting chromosomal translocations - with
PT   sequence complementary to translocation junction-spanning nucleic
PT   acid segment
PS   Disclosure; Page 64; 75pp; English.
CC   The sequences given in Q57092-150 are probes which were used in the
CC   detection of chromosomal translocations.  These oligonucleotides
CC   comprise a nucleotide sequence complementary to that of a
CC   translocation junction-spanning cellular nucleic acid segment where
CC   the translocation is inter- or intra-chromosomal.  These probes may
CC   also be used as primers for detecting chromosomal translocations
CC   associated with diseases, esp. leukemia, sarcoma, lymphoma,
CC   chondrodysplasia, Praeder-Willi syndrome, muscular hypotonia,
CC   incontinentia pigmenti, rhabdo-myosarcoma, trisomy, myelodysplasia,
CC   refractory anaemia, balanced X-autosome, Beckwith-Weidermann syndrome
CC   or endocrine dysplasia.
SQ   Sequence   40 BP;    9 A;    10 C;    9 G;    12 T;

  Query Match           57.7%;  Score 15;  DB 10;  Length 40;
  Best Local Similarity 100.0%;  Pred. No. 3.77e+01;
  Matches   15;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db     26 ctctgcttaaatcca 40
          |||||||||||||||
Cp     26 CTCTGCTTAAATCCA 12


RESULT    6
ID   V39477 standard; DNA; 18 BP.
AC   V39477;
DT   22-SEP-1998  (first entry)
DE   Chronic myelogenous leukaemia capture probe 2MS with mismatches.
KW   Acute lymphocytic leukaemia; Chronic myelogenous leukaemia; ALL; CML;
KW   target; capture probe; detection probe; hybridisation; bcr; abl;
KW   multiple analyte; Salmonella; chromasomal translocation;
KW   Philadelphia chromosome; ss.
OS   Synthetic.
OS   Homo sapiens.
PN   EP-846776-A2.
PD   10-JUN-1998.
PF   05-DEC-1997; 309831.
PR   06-DEC-1996; US-761131.
PA   (VYSI-) VYSIS INC.
PI   Lane DJ, Muller UR;
DR   WPI; 98-299988/27.
PT   Assay device for isolating analyte from sample, e.g. Salmonella in
PT   food - comprises tube containing linear array of binding elements,
PT   linked to binding factor to which component binds
PS   Example 2; Page 12; 25pp; English.
CC   An assay device has been developed for isolating an analyte from a
CC   sample. The assay device comprises a tube containing a linear array of
CC   binding elements, each linked to a distinct binding factor to which a
CC   corresponding specific component binds, where each of the binding
CC   elements is configured to sealingly contact the interior surface of the
CC   tube along the entire circumference of the binding element. The present
CC   sequence represents a capture probe used in an example from the present
CC   invention for the detection of chromosomal translocations. The new
CC   method and device can be used to detect e.g. Salmonella in a food
CC   sample. They are also used to detect chromasomal translocations to
CC   detect the 'Philadelphia' chromosome responsible for acute lymphocytic
CC   leukaemia and chronic myelogenous leukaemia.
SQ   Sequence   18 BP;    5 A;    3 C;    5 G;    5 T;

  Query Match           53.8%;  Score 14;  DB 45;  Length 18;
  Best Local Similarity 88.9%;  Pred. No. 1.23e+02;
  Matches   16;  Conservative    0;  Mismatches   2;  Indels   0;  Gaps   0;

Db      1 taaatgcagtgcctgagt 18
          ||||| ||||| ||||||
Cp     19 TAAATCCAGTGGCTGAGT 2


RESULT    7
ID   Q37186 standard; mRNA; 30 BP.
AC   Q37186;
DT   13-NOV-1992  (first entry)
DE   Bcr-abl mRMA sequence.
KW   Hammerhead; ribozyme; bcr-abl; catalytic domain; target;
KW   cell proliferation; Ph1+; Philadelphia chromosome;
KW   chronic myelogenous leukemia; CML; acute lymphoblastic leukemia;
KW   ALL; ss.
OS   Synthetic.
FH   Key             Location/Qualifiers
FT   misc_feature    19..20
FT                   /*tag=  a
FT                   /label= fusion_site
FT   misc_feature    14..16
FT                   /*tag=  b
FT                   /note= ""hammerhead" catalytic domain target"
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PN   WO9303141-A.
PD   18-FEB-1993.
PF   01-AUG-1991; U05443.
PR   01-AUG-1991; WO-U05443.
PA   (CITY ) CITY OF HOPE.
PI   Forman SJ,  Rossi JJ,  Snyder DS;
DR   WPI; 93-076498/09.
PT   Purging leukaemia cells from bone marrow - by ex vivo treatment
PT   with a ribozyme that inhibits expression of BCR-ABL gene prod.
PS   Disclosure; Fig 1; 30pp; English.
CC   The ribozyme cleaves the bcr-abl mRNA specifically and can inhibit
CC   Ph1+ cell proliferation and/or differentiation.  The ribozyme can
CC   be used to purge leukaemia cells from the bone marrow of patients
CC   with chronic myelogenous leukemia (CML) or acute lymphoblastic
CC   leukemia (ALL), esp. ex vivo.  The purged bone marrow is then used
CC   to reconstitute the patients' haematopoietic system.
SQ   Sequence   30 BP;    10 A;    6 C;    7 G;    7 U;

  Query Match           53.8%;  Score 14;  DB 6;  Length 30;
  Best Local Similarity 78.6%;  Pred. No. 1.23e+02;
  Matches   11;  Conservative    3;  Mismatches   0;  Indels   0;  Gaps   0;

Db       1 ggauuuaagcagag 14
           |||:::|||||||
Qy      13 GGATTTAAGCAGAG 26


RESULT    8
ID   V01787 standard; RNA; 31 BP.
AC   V01787;
DT   04-JUN-1998  (first entry)
DE   Antisense RNA sequence of the specification.
KW   Antisense; inhibitor; gene expression; chromosomal translocation;
KW   translocation point; pharmaceutical composition;
KW   chronic myelogenous leukaemia; acute lymphoblastic leukaemia;
KW   acute myelogenous leukaemia; Non-Hodgkin lymphoma; treatment; ss.
OS   Synthetic.
PN   WO9746672-A2.
PD   11-DEC-1997.
PF   05-JUN-1997; E02923.
PR   05-JUN-1996; EP-109034.
PA   (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PI   Haas R, Kronenwett R, Sczakiel G;
DR   WPI; 98-042181/04.
PT   Nucleic acid molecule containing chromosomal translocation point -
PT   useful to treat chromosomal translocation disorders, e.g. chronic
PT   myelogenous leukaemia
PS   Claim 6; Page 36; 49pp; English.
CC   V01779-804 represent antisense RNA sequences. For long chain antisense
CC   RNA, the association rate with their target RNA in vitro correlates
CC   with their effectiveness in vivo. Antisense molecules are potent
CC   inhibitors of gene expression and viral functions. The antisense
CC   molecules V01779-804 exemplify novel nucleic acid molecules of the
CC   invention. These nucleic acid molecules contain portions complementary to
CC   a first and second chromosomal DNA sequence. The nucleic acid molecule
CC   forms at least part of a chromosomal translocation resulting in a fusion
CC   gene containing the translocation point. The DNA sequence, as well as
CC   vectors and host cells containing it are useful in pharmaceutical
CC   compositions for treating disorders based on chromosomal translocations,
CC   preferably for chronic myelogenous leukaemia. The pharmaceutical
CC   composition may also be used to treat acute lymphoblastic leukaemias,
CC   acute myelogenous leukaemias and Non-Hodgkin lymphomas.
SQ   Sequence   31 BP;    7 A;    7 C;    7 G;    10 U;

  Query Match           53.8%;  Score 14;  DB 40;  Length 31;
  Best Local Similarity 64.3%;  Pred. No. 1.23e+02;
  Matches    9;  Conservative    5;  Mismatches   0;  Indels   0;  Gaps   0;

Db      18 cucugcuuaaaucc 31
           |:|:||::|||:||
Cp      26 CTCTGCTTAAATCC 13


RESULT    9
ID   N81469 standard; DNA; 17 BP.
AC   N81469;
DT   15-OCT-1990  (first entry)
DE   Probe to B-cell differentiation factor (BCDF) encoding gene.
KW   B-cell differentiation factor; BCDF; cancer; autoimmune.
OS   Homo sapiens.
PN   EP-257406-A.
PD   2-MAR-1988.
PF   6-AUG-1988; 111409.
PR   06-AUG-1986; JP-184858.
PR   27-AUG-1986; JP-200433
PR   18-DEC-1986; JP-302699.
PR   13-MAY-1987; JP-116332.
PA   (AJIN) Ajinomoto KK.
PI   Kishimoto TN, Hirano T, Matsui H, Takahara Y, Akiyama Y, Okano A;
DR   WPI; 88-057698/09.
PT   Purified polypeptide with B-cell differentiation factor activity -
PT   useful in prodn. of antibodies for diagnosis and therapy of
PT   cancers, infectious diseases etc.
PS   Example 3; Page 15-16; 72pp; English.
CC   Probe is used to generate peptide with BCDF activity, which
CC   may be used in the production and repair of B-cells. Also
CC   useful in treatment of autoimmune diseases, malignant tumors
CC   and may be used to influence B-cells to produce Abs in vitro.
SQ   Sequence   17 BP;    4 A;    3 C;    3 G;    2 T;    5 Others;

  Query Match           50.0%;  Score 13;  DB 1;  Length 17;
  Best Local Similarity 58.8%;  Pred. No. 3.86e+02;
  Matches   10;  Conservative    5;  Mismatches   2;  Indels   0;  Gaps   0;

Db       1 gcycaraaycartggyt 17
           ||: |:| :||:|||:|
Cp      22 GCTTAAATCCAGTGGCT 6


RESULT   10
ID   Q56274 standard; DNA; 17 BP.
AC   Q56274;
DT   15-SEP-1994  (first entry)
DE   Sequence of Probe No. 8-2 based on B-cell differentiation factor
DE   fragment (BCDF) no. 8.
KW   B-cell differentiation factor; BCDF; antitumour; antiviral;
KW   lymphokine; ss.
OS   Synthetic.
PN   EP-585957-A.
PD   09-MAR-1994.
PF   06-AUG-1987; 111409.
PR   06-AUG-1986; JP-184858.
PR   27-AUG-1986; JP-200433.
PR   18-DEC-1986; JP-302699.
PR   13-MAY-1987; JP-116332.
PA   (AJIN ) AJINOMOTO KK.
PA   (KISH/) KISHIMOTO T.
PI   Akiyama Y,  Hirano T,  Kishimoto T,  Matsui H,  Okano A;
PI   Takahara Y;
DR   WPI; 94-076278/10.
PT   New non-glycosylated human B-cell differentiation factor -
PT   lacking signal sequence and produced in bacteria, useful as
PT   immuno therapeutic for stimulating antibody prodn, treating
PT   cancer etc, also DNA encoding it
PS   Example; Page 15; 63pp; English.
CC   Human T cells transformed by human T cell leukaemia virus (HTLV)
CC   produce BCDF. BCDF was prepd. from the supernatant of cultured
CC   VT-1 cells. The N-terminal sequence was determined to be:
CC   PVPPGEDSKDVAA. The BCDF prepn. was digested with Lysyl
CC   endopeptidase. The resultant fragment 3 has the sequence:
CC   KEALAE. The resultant fragment 8 has the sequence: KLXAQNEWLQXM.
CC   Q56267-Q56274 show the sequences of mixtures of probes based
CC   on Fragment 3, Fragment 8 and the N-terminal AA sequence of
CC   BCDF.
SQ   Sequence   17 BP;    4 A;    3 C;    3 G;    2 T;
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  Query Match           50.0%;  Score 13;  DB 10;  Length 17;
  Best Local Similarity  58.8%;  Pred. No. 3.86e+02;
  Matches    10;  Conservative    5;  Mismatches   2;  Indels   0;  Gaps   0;

Db      1 gcycaraaycartggyt 17
          ||: |:| :||:|||:|
Cp     22 GCTTAAATCCAGTGGCT 6


RESULT   11
ID   Q51833 standard; RNA; 18 BP.
AC   Q51833;
DT   26-MAY-1994  (first entry)
DE   bcr mRNA ribozyme cleavable nucleotide 3360.
KW   Multiple drug resistance; mdr-1; ribozyme; membrane protein; liver;
KW   resistance; chemotherapeutic agent; colchicine; doxorubicin; colon;
KW   actinomycin D; vinblastine; small intestine; kidney; adrenal gland;
KW   adenocarcinoma; bowel; transformed phenotype; promyelocytic leukemia;
KW   human; chronic myelogenous leukemia; CML; follicular lymphoma;
KW   B-cell acute lymphocytic leukemia; breast cancer; colon carcinoma;
KW   neuroblastoma; lung cancer; genetic drift; mutation; hammerhead motif;
KW   hairpin; hepatitis delta virus; group I intron; RNaseP; ss.
OS   Homo sapiens.
PN   WO9323057-A.
PD   25-NOV-1993.
PF   13-MAY-1993; U04573.
PR   14-MAY-1992; US-882822.
PR   14-MAY-1992; US-882885.
PR   26-AUG-1992; US-936421.
PR   26-AUG-1992; US-936110.
PR   26-AUG-1992; US-936422.
PR   26-AUG-1992; US-936532.
PR   26-AUG-1992; US-936531.
PR   07-DEC-1992; US-987131.
PR   19-JAN-1993; US-006122.
PR   19-JAN-1993; US-008910.
PA   (RIBO-) RIBOZYME PHARM INC.
PI   Draper KG,  Thompson JD;
DR   WPI; 93-386203/48.
PT   New enzymatic RNA molecules (ribozymes) - which cleave mRNA
PT   associated with tumours or mRNA expressed from gene encoding
PT   multiple drug resistance
PS   Claim 3; Fig 3; 69pp; English.
CC   The sequences given in Q51825-2266 represent areas of mRNAs
CC   associated with development or maintenance of chronic myelogenous
CC   leukemia (CML), promyelocytic leukemia, Burkitt's lymphoma, or
CC   acute lymphocytic leukemia, follicular lymphoma, B-cell acute
CC   lymphocytic leukemia, breast cancer, colon carcinoma, neuroblastoma
CC   and lung cancer.  The full length mRNAs containing these target
CC   sequences, encode aberant cellular proteins which are able to control
CC   cellular proliferation and are directly linked to a leukemic
CC   phenotype.  These target sequences are identified by the ribozyme of
CC   the invention.  The ribozymes is formed in a hammerhead motif, but may
CC   also be formed in the motif of a hairpin, hepatitis delta virus, group
CC   I intron or RNaseP-like RNA.  These ribozymes may be used to inhibit
CC   the development or expression of a transformed phenotype in man and
CC   other animals by modulating expression of the corresponding gene.
CC   Cleavage of target mRNAs expressed in pre-neoplastic and transformed
CC   cells elicits inhibition of the transformed state.  Multiple drug
CC   resistance (mdr-1) mRNA specific ribozymes remove the mechanism of
CC   drug resistance used by transformed cells and thus enhances drug
CC   therapies for tumours.  The ribozymes may also be used to study
CC   genetic drift and mutations within cells.
SQ   Sequence   18 BP;    7 A;    2 C;    4 G;    5 U;

  Query Match           50.0%;  Score 13;  DB 9;  Length 18;
  Best Local Similarity  76.9%;  Pred. No. 3.86e+02;
  Matches    10;  Conservative    3;  Mismatches   0;  Indels   0;  Gaps   0;

Db      1 gauuuaagcagag 13
          ||:::|||||||
Qy     14 GATTTAAGCAGAG 26


RESULT   12
ID   Q34636 standard; cDNA; 22 BP.
AC   Q34636;
DT   10-MAY-1993  (first entry)
DE   Human bcr exon 3 5' PCR primer.
KW   Leukaemia; treatment; blast crisis; specific; CML; translocation;
KW   Philadelphia chromosome; chronic myeloid; chronic myelogenous;
KW   leukemia; polymerase chain reaction; ss.
OS   Synthetic.
PN   WO9222303-A.
PD   23-DEC-1992.
PF   15-JUN-1992; U05035.
PR   18-JUN-1991; US-718302.
PR   14-APR-1992; US-869911.
PA   (UTEM ) UNIV TEMPLE.
PI   Calabretta B, Gewirtz AM;
DR   WPI; 93-017893/02.
PT   Treating Ph1-positive leukaemia(s) using bcr-abl anti-sense oligo-
PT   nucleotide(s) - to selectively inhibit leukaemic cell proliferation
PT   without adversely affecting normal haematopoiesis
PS   Disclosure; Page 51; 74pp; English.
CC   The sequence is that of the 5' primer complementary to 22 nucleotides
CC   of bcr exon 3 which was used to amplify RNA derived from cells
CC   of CML patients in blast crisis to obtain the sequence of the b3a2
CC   junction. It was used as part of a method to treat leukaemias
CC   characterised by the Philadelphia chromosome translocation. It is
CC   highly selective and patient specific unlike conventional chemotherapy,
CC   which affects non-malignant cells. Dosage selection is thus less
CC   critical than with conventional treatment.
SQ   Sequence   22 BP;    4 A;    9 C;    4 G;    5 T;

  Query Match           50.0%;  Score 13;  DB 6;  Length 22;
  Best Local Similarity 100.0%;  Pred. No. 3.86e+02;
  Matches    13;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db     10 cactcagccactg 22
          |||||||||||||
Qy      1 CACTCAGCCACTG 13


RESULT   13
ID   V01786 standard; RNA; 30 BP.
AC   V01786;
DT   04-JUN-1998  (first entry)
DE   Antisense RNA sequence of the specification.
KW   Antisense; inhibitor; gene expression; chromosomal translocation;
KW   translocation point; pharmaceutical composition;
KW   chronic myelogenous leukaemia; acute lymphoblastic leukaemia;
KW   acute myelogenous leukaemia; Non-Hodgkin lymphoma; treatment; ss.
OS   Synthetic.
PN   WO9746672-A2.
PD   11-DEC-1997.
PF   05-JUN-1997; E02923.
PR   05-JUN-1996; EP-109034.
PA   (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PI   Haas R, Kronenwett R, Sczakiel G;
DR   WPI; 98-042181/04.
PT   Nucleic acid molecule containing chromosomal translocation point -
PT   useful to treat chromosomal translocation disorders, e.g. chronic
PT   myelogenous leukaemia
PS   Claim 6; Page 36; 49pp; English.
CC   V01779-804 represent antisense RNA sequences. For long chain antisense
CC   RNA, the association rate with their target RNA in vitro correlates
CC   with their effectiveness in vivo. Antisense molecules are potent
CC   inhibitors of gene expression and viral functions. The antisense
CC   molecules V01779-804 exemplify novel nucleic acid molecules of the
CC   invention. These nucleic acid molecules contain portions complementary to
CC   a first and second chromosomal DNA sequence. The nucleic acid molecule
CC   forms at least part of a chromosomal translocation resulting in a fusion
CC   gene containing the translocation point. The DNA sequence, as well as
CC   vectors and host cells containing it are useful in pharmaceutical
CC   compositions for treating disorders based on chromosomal translocations,
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CC   preferably for chronic myelogenous leukaemia. The pharmaceutical
CC   composition may also be used to treat acute lymphoblastic leukaemias,
CC   acute myelogenous leukaemias and Non-Hodgkin lymphomas.
SQ   Sequence   30 BP;    7 A;    6 C;    7 G;    10 U;

  Query Match           50.0%;  Score 13;  DB 40;  Length 30;
  Best Local Similarity 61.5%;  Pred. No. 3.86e+02;
  Matches    8;  Conservative    5;  Mismatches   0;  Indels   0;  Gaps   0;

Db     18 cucugcuuaaauc 30
          |:|:||::|||:|
Cp     26 CTCTGCTTAAATC 14


RESULT   14
ID   V01804 standard; RNA; 40 BP.
AC   V01804;
DT   04-JUN-1998  (first entry)
DE   Antisense RNA sequence of the specification.
KW   Antisense; inhibitor; gene expression; chromosomal translocation;
KW   translocation point; pharmaceutical composition;
KW   chronic myelogenous leukaemia; acute lymphoblastic leukaemia;
KW   acute myelogenous leukaemia; Non-Hodgkin lymphoma; treatment; ss.
OS   Synthetic.
PN   WO9746672-A2.
PD   11-DEC-1997.
PF   05-JUN-1997; E02923.
PR   05-JUN-1996; EP-109034.
PA   (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PI   Haas R, Kronenwett R, Sczakiel G;
DR   WPI; 98-042181/04.
PT   Nucleic acid molecule containing chromosomal translocation point -
PT   useful to treat chromosomal translocation disorders, e.g. chronic
PT   myelogenous leukaemia
PS   Claim 6; Page 37; 49pp; English.
CC   V01779-804 represent antisense RNA sequences. For long chain antisense
CC   RNA, the association rate with their target RNA in vitro correlates
CC   with their effectiveness in vivo. Antisense molecules are potent
CC   inhibitors of gene expression and viral functions. The antisense
CC   molecules V01779-804 exemplify novel nucleic acid molecules of the
CC   invention. These nucleic acid molecules contain portions complementary to
CC   a first and second chromosomal DNA sequence. The nucleic acid molecule
CC   forms at least part of a chromosomal translocation resulting in a fusion
CC   gene containing the translocation point. The DNA sequence, as well as
CC   vectors and host cells containing it are useful in pharmaceutical
CC   compositions for treating disorders based on chromosomal translocations,
CC   preferably for chronic myelogenous leukaemia. The pharmaceutical
CC   composition may also be used to treat acute lymphoblastic leukaemias,
CC   acute myelogenous leukaemias and Non-Hodgkin lymphomas.
SQ   Sequence   40 BP;    8 A;    10 C;    10 G;    12 U;

  Query Match           50.0%;  Score 13;  DB 40;  Length 40;
  Best Local Similarity 61.5%;  Pred. No. 3.86e+02;
  Matches    8;  Conservative    5;  Mismatches   0;  Indels   0;  Gaps   0;

Db     28 cucugcuuaaauc 40
          |:|:||::|||:|
Cp     26 CTCTGCTTAAATC 14


RESULT   15
ID   V97763 standard; RNA; 17 BP.
AC   V97763;
DT   17-MAR-1999  (first entry)
DE   Human EGF-R target sequence nucleotide position 4299.
KW   Human; epidermal growth factor receptor; EGFR; EGF-R; target sequence;
KW   hammerhead ribozyme; hairpin ribozyme; inhibition; cell proliferation;
KW   cancer; genetic drift; detection; mutation; ss.
OS   Homo sapiens.
PN   WO9833893-A2.
PD   06-AUG-1998.
PF   14-JAN-1998; U00730.
PR   04-DEC-1997; US-985162.
PR   31-JAN-1997; US-036476.
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (UYAS-) UNIV ASTON.
PI   Akhtar S, Fell P, McSwiggen JA;
DR   WPI; 98-437449/37.
PT   Enzymatic nucleic acids - which cleave RNA derived from an epidermal
PT   growth factor receptor, useful for inhibiting cell proliferation and
PT   for treating cancers
PS   Claim 5; Page 79; 109pp; English.
CC   The present invention describes enzymatic nucleic acid molecules (NAMs)
CC   which specifically cleave RNA derived from an epidermal growth factor
CC   receptor (EGF-R) gene. V97221 to V98043 and V98979 to V99090 represent
CC   specifically claimed target sequence from human EGF-R. V98044 to v98866
CC   and V98867 to V9878 represent hammerhead ribozymes and hairpin ribozymes
CC   respectively for human EGF-R. The NAMs are useful for cleaving EGF-R RNA
CC   in the treatment of a condition associated with EGFR expression levels
CC   e.g. to inhibit cell proliferation in the prevention or treatment of
CC   cancers. The NAMs can also be used as diagnostic tools to examine
CC   genetic drift and mutations within diseased cells or to detect the
CC   presence of EGF-R RNA in a cell.
SQ   Sequence   17 BP;    2 A;    3 C;    5 G;    7 U;

  Query Match           46.2%;  Score 12;  DB 59;  Length 17;
  Best Local Similarity 56.3%;  Pred. No. 1.16e+03;
  Matches    9;  Conservative    5;  Mismatches   2;  Indels   0;  Gaps   0;

Db      1 ugcuugauuccagugg 16
          :||:: | :||||:||
Cp     23 TGCTTAAATCCAGTGG 8


RESULT   16
ID   Q14330 standard; DNA; 18 BP.
AC   Q14330;
DT   15-JAN-1992  (first entry)
DE   MCPC 603 VL CDR1 walk-through mutagenesis oligonucleotide (Ser, His).
KW   Mutagenesis; monoclonal antibody; Fv molecule; ss.
OS   Synthetic.
PN   WO9115581-A.
PD   17-OCT-1991.
PF   05-APR-1991; U02362.
PR   05-APR-1990; US-505314.
PA   (CREA/) CREA R.
PI   Crea R;
DR   WPI; 91-325224/44.
PT   Walk-through mutagenesis of proteins - by introducing predetermined
PT   amino acid in each sequence position in preselected region of the
PT   protein
PS   Disclosure; Fig 8A; 91pp; English.
CC   Walk-through mutagenesis of five out of six CDRs of the MCPC 603 Fv
CC   molecule is performed, and Asp, His and Ser are the preselected amino
CC   acids.  In this model, walk-through mutagenesis is carried out from two
CC   to three times with a different amino acid in a given region or domain.
CC   For example, Ser and His are sequentially walked-through VL CDR1, and
CC   Asp and Ser are sequentially walked-through VL CDR3 (Q14331).
CC   VL CDR2 was not targeted for mutagenesis because structural studies
CC   indicated that this region contributes little to the binding site in
CC   MCPC 603.  In CDR1 of the VH chain of the Fv, Asp and His are walked
CC   through (Q14332).  Ser can be introduced at two positions in CDR1
CC   with a single base change.  In VH CDR2, His and Ser are the
CC   preselected amino acids used (Q14333) and in VH CDR3, Asp, His and
CC   Ser are each walked through the amino terminal five positions of
CC   CDR3 (Q14334).
CC   See also Q14321-34.
SQ   Sequence   18 BP;    0 A;    3 C;    1 G;    2 T;

  Query Match           46.2%;  Score 12;  DB 3;  Length 18;
  Best Local Similarity 28.6%;  Pred. No. 1.16e+03;
  Matches    4;  Conservative    9;  Mismatches   1;  Indels   0;  Gaps   0;

Db      5 mkmrkyhcctgsht 18
          ::::::: |||::|
Qy      3 CTCAGCCACTGGAT 16
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RESULT   17
ID   Q28817 standard; DNA; 21 BP.
AC   Q28817;
DT   26-FEB-1993  (first entry)
DE   HLA Class II gene locus PCR primer DQB6.
KW   Polymerase chain reaction; MHC genotype; human leukocyte antigen;
KW   major histocompatibility complex; automated determination; ss.
OS   Synthetic.
PN   WO9215711-A.
PD   17-SEP-1992.
PF   04-MAR-1992; U01675.
PR   06-MAR-1991; US-665960.
PR   18-FEB-1992; US-833668.
PA   (MINU ) UNIV MINNESOTA.
PI   Barbosa JJ, Boyce-Jacino MT, Faras AJ, Rich SS, Santamaria P;
DR   WPI; 92-331755/40.
PT   Fully automated determn. of MHC genotype - by isolating nucleic
PT   acid from sample, amplifying nucleic acid by PCR to sequence
PT   alleles and analysing sequenced prods.
PS   Example; Page 22; 105pp; English.
CC   The sequence is that of a PCR primer used as part of a method for
CC   determining the major histocompatibility complex (MHC) genotype of
CC   a subject in a sample. The primer anneals to nucleotides -8/-2 of
CC   HLA class II locus DQB1.
CC   See also Q28761-Q28800 and Q28811-Q28819.
SQ   Sequence   21 BP;   4 A;   7 C;   7 G;   3 T;

  Query Match          46.2%;  Score 12;  DB 5;  Length 21;
  Best Local Similarity 100.0%;  Pred. No. 1.16e+03;
  Matches   12;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Db      10 ccagtggctgag 21
           ||||||||||||
Cp      14 CCAGTGGCTGAG 3


RESULT   18
ID   Q74572 standard; RNA; 28 BP.
AC   Q74572;
DT   05-MAY-1995  (first entry)
DE   Probe for the detection of HIV-1.
KW   Probe; primer; detection; amplification; identification; diagnosis;
KW   HIV-1; human immunodeficiency virus; HTLV-1; AIDS;
KW   human T-cell leukaemia virus; acquired immune deficiency syndrome;
KW   ss.
OS   Synthetic.
PN   EP-617132-A.
PD   28-SEP-1994.
PF   28-MAR-1994; 302196.
PR   26-MAR-1993; US-040745.
PA   (GENP-) GEN-PROBE INC.
PI   Mcdonough SH,  Ryder TB,  Yang Y;
DR   WPI; 94-295780/37.
PT   New oligonucleotides corresponding to HIV-1 sequences - used for
PT   selective amplification and as hybridisation probes for detection
PT   of HIV-1.
PS   Claim 1; Page 51; 69pp; English.
CC   Probes and primers specific for HIV-1 were identified by comparison
CC   of published sequences of HIV-1, HIV-2, HTLV-1 and HTLV-2 and were
CC   then synthesised. The probes are able to detect HIV-1 in a sample
CC   and distinguish it from its known closest phylogenetic neighbours.
CC   See Q74533-Q74574.
SQ   Sequence   28 BP;   7 A;   10 C;   5 G;   6 U;

  Query Match          46.2%;  Score 12;  DB 12;  Length 28;
  Best Local Similarity 59.1%;  Pred. No. 1.16e+03;
  Matches   13;  Conservative   4;  Mismatches   5;  Indels   0;  Gaps   0;

Db       3 cucagauccugcauauaagcag 24
           |:|||   |:| |: :|||||||
Qy       3 CTCAGCCACTGGATTTAAGCAG 24


RESULT   19
ID   Q74497 standard; DNA; 28 BP.
AC   Q74497;
DT   04-MAY-1995  (first entry)
DE   Probe for the detection of HIV-1.
KW   Probe; primer; detection; amplification; identification; diagnosis;
KW   HIV-1; human immunodeficiency virus; HTLV-1; AIDS;
KW   human T-cell leukaemia virus; acquired immune deficiency syndrome;
KW   ss.
OS   Synthetic.
PN   EP-617132-A.
PD   28-SEP-1994.
PF   28-MAR-1994; 302196.
PR   26-MAR-1993; US-040745.
PA   (GENP-) GEN-PROBE INC.
PI   Mcdonough SH,  Ryder TB,  Yang Y;
DR   WPI; 94-295780/37.
PT   New oligonucleotides corresponding to HIV-1 sequences - used for
PT   selective amplification and as hybridisation probes for detection
PT   of HIV-1.
PS   Claim 1; Page 3; 69pp; English.
CC   Probes and primers specific for HIV-1 were identified by comparison
CC   of published sequences of HIV-1, HIV-2, HTLV-1 and HTLV-2 and were
CC   then synthesised. The probes are able to detect HIV-1 in a sample
CC   and distinguish it from its known closest phylogenetic neighbours.
CC   See Q74486-Q74499.
SQ   Sequence   28 BP;   6 A;   5 C;   10 G;   7 T;

  Query Match          46.2%;  Score 12;  DB 12;  Length 28;
  Best Local Similarity 77.3%;  Pred. No. 1.16e+03;
  Matches   17;  Conservative   0;  Mismatches   5;  Indels   0;  Gaps   0;

Db       5 ctgcttatatgcaggatctgag 26
           ||||||| || |||   |||||
Cp      24 CTGCTTAAATCCAGTGGCTGAG 3


RESULT   20
ID   Q86609 standard; DNA; 28 BP.
AC   Q86609;
DT   15-NOV-1995  (first entry)
DE   Human immunodeficiency virus (HIV) region 1 probe.
KW   Primer; autocatalytic; target; HIV; ss.
OS   Synthetic.
PN   US5399491-A.
PD   21-MAR-1995.
PF   11-JUL-1989; 379501.
PR   11-JUL-1989; US-379501.
PR   10-JUL-1990; US-550837.
PR   19-MAR-1992; US-855732.
PA   (GENP-) GEN-PROBE INC.
PI   Fultz TJ,  Kacian DL;
DR   WPI; 95-130686/17.
PT   Amplification of nucleic acid targets - using a reverse
PT   transcriptase with RNase H activity and a RNA polymerase at
PT   constant temp.
PS   Disclosure; Column 9; 58pp; English.
CC   Q86607-09 are primers and a probe for the human immunodeficiency
CC   virus region 1. They are used to produce autocatalytic
CC   oligonucleotides which require no change in the experimental
CC   conditions i.e.constant temperature, pH and ionic strength.
CC   These sequences are useful in generating multiple copies of
CC   specific nucleic acid target sequences.
SQ   Sequence   28 BP;   6 A;   5 C;   10 G;   7 T;

  Query Match          46.2%;  Score 12;  DB 15;  Length 28;
  Best Local Similarity 77.3%;  Pred. No. 1.16e+03;
  Matches   17;  Conservative   0;  Mismatches   5;  Indels   0;  Gaps   0;

Db       5 ctgcttatatgcaggatctgag 26
           ||||||| || :||   |||||
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Cp     24 CTGCTTAAATCCAGTGGCTGAG 3


RESULT   21
ID   V92356 standard; RNA; 29 BP.
AC   V92356;
DT   18-FEB-1999  (first entry)
DE   Human A-Raf hammerhead ribozyme position 2347.
KW   Human; c-raf; A-raf; B-raf; hammerhead ribozyme; hairpin ribozyme;
KW   target; substrate; catalyst; modulation; expression; Raf gene;
KW   delivery; screening; identification; synthesis; deprotection;
KW   purification; cancer; inflammation; psoriasis; non-hepatic ascites;
KW   infection; genetic drift; restenosis; rheumatoid arthritis; ss.
OS   Synthetic.
OS   Homo sapiens.
PN   WO9850530-A2.
PD   12-NOV-1998.
PF   05-MAY-1998; U09249.
PR   19-DEC-1997; US-068212.
PR   09-MAY-1997; US-046059.
PR   09-JUN-1997; US-049002.
PR   03-JUL-1997; US-051718.
PR   22-AUG-1997; US-056808.
PR   02-OCT-1997; US-061321.
PR   02-OCT-1997; US-061324.
PR   05-NOV-1997; US-064866.
PA   (RIBO-) RIBOZYME PHARM INC.
PI   Beaudry A, Beigelman L, Bellon L, Burgin A, Jarvis T,
PI   Karpeisky A, Kisich K, Matulic-Adamic J, McSwiggen JA,
PI   Parry T, Reynolds M, Sweedler D, Thompson J, Workman CT;
DR   WPI; 99-009494/01.
PT   Identifying new catalytic nucleic acid that modulates selected
PT   processes - especially ribozymes that cleave Raf RNA for treating
PT   cancer, restenosis, and also new ribozymes and modified nucleoside
PT   triphosphates used as antiviral agents and synthons
PS   Claim 151; Page 162; 259pp; English.
CC   A method has been developed for the identification of a nucleic acid
CC   capable of modulating a process in a biological system. The method
CC   comprises: (a) introducing into the system a random library of nucleic
CC   acid catalysts (NAC) having a substrate binding domain (SBD), comprising
CC   a random sequence, and a catalytic domain (CD); and (b) identifying NAC
CC   in systems where modulation has occurred and/or determining the sequence
CC   of at least part of the SBDs in such systems. Nucleic acid molecules with
CC   endonuclease activity and catalytic activity, from the present invention,
CC   are used to modulate gene expression in plant and mammalian cells and to
CC   cleave target nucleic acid, particularly for treating systemic diseases
CC   caused by specific RNA, e.g. cancer, inflammation, psoriasis, non-hepatic
CC   ascites and infection. They may also be used to detect genetic drift and
CC   mutations in diseased cells and to determine c-raf RNA. Specifically NACs
CC   with RNA-cleaving activity that modulate expression of the Raf gene, are
CC   used to treat cancer, restenosis, psoriasis or rheumatoid arthritis, or
CC   generally any condition associated with the level of c-raf. Introduction
CC   of sugar/phosphate modifications increases stability against nuclease
CC   and activity. V90922 to V93877 represent NACs that can be used in the
CC   method, specifically for modulating the expression of a Raf gene.
SQ   Sequence   29 BP;    8 A;    6 C;    9 G;    5 U;

  Query Match           46.2%;  Score 12;  DB 56;  Length 29;
  Best Local Similarity  75.0%;  Pred. No. 1.16e+03;
  Matches     9;  Conservative    3;  Mismatches   0;  Indels   0;  Gaps   0;

Db      1 uccaguggcuga 12
          :||||:|||:||
Cp     15 TCCAGTGGCTGA 4


RESULT   22
ID   Q46735 standard; DNA; 33 BP.
AC   Q46735;
DT   16-DEC-1993  (first entry)
DE   HIV amplifier probe HIV.151.
KW   Probe; hybridisation; assay; detection;
KW   human immunodeficiency virus; HIV; human lymphotrophic retrovirus;
KW   solution phase; comb-type branched polynucleotide; sidechain;
KW   extension; binding site; ligation; template; linker; ss.
OS   Synthetic.
PN   WO9313223-A.
PD   08-JUL-1993.
PF   22-DEC-1992; U11168.
PR   23-DEC-1991; US-813583.
PA   (CHIR ) CHIRON CORP.
PI   Irvine BD,  Kolberg JA,  Urdea MS;
DR   WPI; 93-227337/28.
PT   Synthetic oligo:nucleotide useful as amplifier probe for HIV
PT   detection - comprises 1st segment complementary to HIV sequence
PT   and 2nd segment complementary to oligo unit of nucleic acid
PT   multimer
PS   Claim 1; Page 73; 92pp; English.
CC   A "15 x 3" amplified soln. phase nucleic acid sandwich hybridisation
CC   assay employs two multimers: (1) an amplifier probe having a first
CC   segment (A) that binds to HIV and a second segment (B) that
CC   hybridises to (2) an amplifier multimer having a first segment (B*)
CC   that hybridises to the segment (B) and fifteen iterations of a
CC   segment (C), wherein segment C hybridises to three labeled
CC   oligonucleotides.
CC   HIV amplifier probes are given in Q46703-742.
CC   HIV capture probes are given in Q46743-752.
CC   Each amplifier probe contained, in addition to the sequences
CC   complementary to the HIV sequences, the 5' extension given in
CC   Q46753, complementary to a segment of the amplifier multimer.
CC   Each capture probe contained, in addition to the sequences
CC   complementary to the HIV sequences, a downstream sequence given
CC   in Q46754, complementary to the DNA bound to the solid phase.
CC   In addition to the amplifier and capture probes, a set of HIV
CC   spacer oligonucleotides (Q46755-61) was included in the
CC   hybridisation mixt.
SQ   Sequence   33 BP;    7 A;    11 C;    3 G;    7 T;

  Query Match           46.2%;  Score 12;  DB 7;  Length 33;
  Best Local Similarity  64.3%;  Pred. No. 1.16e+03;
  Matches     9;  Conservative    4;  Mismatches   1;  Indels   0;  Gaps   0;

Db      14 ctgyttrathcchg 27
             |||:||:| :||:|
Cp      24 CTGCTTAAATCCAG 11


RESULT   23
ID   Q89511 standard; cDNA; 33 BP.
AC   Q89511;
DT   04-DEC-1995  (first entry)
DE   Human immunodeficiency virus (HIV) probe.
KW   Human immunodeficency virus; HIV; probe; nucleotide; hybridisation;
KW   ss.
OS   Synthetic.
PN   USH001431-H.
PD   04-APR-1995.
PF   04-NOV-1992; 971719.
PR   04-NOV-1992; US-971719.
PA   (KERN/) KERN D G.
PA   (SHER/) SHERIDAN P J.
PA   (TODD/) TODD J.
PI   Kern DG,  Sheridan PJ,  Todd J;
DR   WPI; 95-146201/19.
PT   Facilitating sepn. of pellet and supernatant in centrifuged sample -
PT   in nucleotide hybridisation assays, by adding beads to the sample to
PT   assist identification of the pellet area, improves precision
PS   Example 1; Column 8; 17pp; English.
CC   Q89479-Q89518 are HIV specific labelled probes which can be used in
CC   a nucleotide hybridisation assay (NHA). The assay demonstrates a new
CC   method using "beads" in sample preparation which increases the
CC   precision of NHAs.
SQ   Sequence   33 BP;    7 A;    11 C;    3 G;    7 T;

  Query Match           46.2%;  Score 12;  DB 15;  Length 33;
  Best Local Similarity  64.3%;  Pred. No. 1.16e+03;
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  Matches    9;  Conservative    4;  Mismatches   1;  Indels   0;  Gaps   0;

Db      14 ctgyttrathcchg 27
           |||:||:| :||:|
Cp      24 CTGCTTAAATCCAG 11


RESULT   24
ID   Q86488 standard; cDNA; 34 BP.
AC   Q86488;
DT   24-NOV-1995  (first entry)
DE   Primer, e24, for amplification of E2F-1 DNA binding region.
KW   Primer; E2F-1; E2F-2; transcription; factor; retinoblastoma; pRb;
KW   tumour; suppressor; ss.
OS   Synthetic.
PN   GB2282814-A.
PD   19-APR-1995.
PF   07-OCT-1994; 020283.
PR   13-OCT-1993; US-136119.
PA   (MERI ) MERCK & CO INC.
PI   Heimbrook DC,  Ivey-Hoyle M,  Oliff AI;
DR   WPI; 95-141220/19.
PT   New human transcription factor E2F-2  - involved in cell cycle
PT   regulation and useful for drug screening, also related cDNA,
PT   plasmids and transformed cells.
PS   Example 1; Page 15; 53pp; English.
CC   Q86484-91 correspond to the E2F-1 primers e20-27 and f120
CC   respectively. The amplified E2F-1 DNA binding region is
CC   substantially complementary to the E2F-2 coding region and is
CC   used as a probe for this region. E2F-2 is involved in cell cycle
CC   regulation. In particular binding of E2F to the retinoblastoma
CC   gene product (pRb) causes down regulation of the transcription
CC   of any genes containing the E2F binding site. E2F-2 is useful in
CC   the study of cell cycle regulation especially in the study
CC   of pRb and certain viral oncogenes and oncoproteins.
SQ   Sequence   34 BP;    6 A;    7 C;    11 G;    10 T;

  Query Match           46.2%;  Score 12;  DB 15;  Length 34;
  Best Local Similarity 100.0%;  Pred. No. 1.16e+03;
  Matches    12;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db      12 cagccactggat 23
           ||||||||||||
Qy       5 CAGCCACTGGAT 16


RESULT   25
ID   Q25115 standard; DNA; 36 BP.
AC   Q25115;
DT   23-NOV-1992  (first entry)
DE   PCR primer 21/M6.
KW   TNF; tumour necrosis factor; mutein; P75; P55; receptor;
KW   amplification; polymerase chain reaction; ss.
OS   Synthetic.
FH   Key             Location/Qualifiers
FT   mutation        7..9
FT                   /*tag=  a
FT   mutation        11..12
FT                   /*tag=  b
PN   EP-486908-A.
PD   27-MAY-1992.
PF   11-NOV-1991; 119128.
PR   21-NOV-1990; EP-810901.
PA   (HOFF ) HOFFMANN LA ROCHE & CO AG F.
PI   Fiers W, Tavernier J, Van Ostadex;
DR   WPI; 92-176547/22.
PT   Human tumour necrosis factor muteins - show difference in binding
PT   affinity to P75 and P55 TNF receptors, for treatment of tumours
PS   Example 7; Page 18; 38pp; English.
CC   The oligomer sequence corresponds to the complement of nucleotides
CC   219-184 of the TNF plasmid pDS56/RBSII,SphI-TNF-alpha (mutated
CC   bases are given in the features table).  The primer 21/M6 was used
CC   in one of three PCR reactions to generate mutant forms of TNF-alpha
CC   e.g. Glu31-TNF and Asn31-Thr32-TNF.  The muteins displays a difference
CC   in binding affinity to P75 and P55 TNF receptors and are useful in
CC   pharmaceutical compsns. in conjunction with non-toxic carrier
CC   molecules for the treatment of e.g. cancer.
CC   See also Q25113-9.
SQ   Sequence   36 BP;    5 A;    11 C;    10 G;    10 T;

  Query Match           46.2%;  Score 12;  DB 4;  Length 36;
  Best Local Similarity 100.0%;  Pred. No. 1.16e+03;
  Matches    12;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db      15 tcagccactgga 26
           ||||||||||||
Qy       4 TCAGCCACTGGA 15


RESULT   26
ID   Q25114 standard; DNA; 36 BP.
AC   Q25114;
DT   23-NOV-1992  (first entry)
DE   PCR primer 21/M5.
KW   TNF; tumour necrosis factor; mutein; P75; P55; receptor;
KW   amplification; polymerase chain reaction; ss.
OS   Synthetic.
FH   Key             Location/Qualifiers
FT   mutation        10..12
FT                   /*tag=  a
FT                   /note= "mutation site"
PN   EP-486908-A.
PD   27-MAY-1992.
PF   11-NOV-1991; 119128.
PR   21-NOV-1990; EP-810901.
PA   (HOFF ) HOFFMANN LA ROCHE & CO AG F.
PI   Fiers W, Tavernier J, Van Ostadex;
DR   WPI; 92-176547/22.
PT   Human tumour necrosis factor muteins - show difference in binding
PT   affinity to P75 and P55 TNF receptors, for treatment of tumours
PS   Example 7; Page 18; 38pp; English.
CC   The oligomer sequence corresponds to the complement of nucleotides
CC   219-184 of the TNF plasmid pDS56/RBSII,SphI-TNF-alpha.  The primer
CC   21/M5 was used in one of three PCR reactions to generate mutant forms
CC   of TNF-alpha e.g. Glu31-TNF and Asn31-Thr32-TNF.  The muteins display
CC   a difference in binding affinity to P75 and P55 TNF receptors and are
CC   useful in pharmaceutical compsns. in conjunction with non-toxic carrier
CC   molecules for the treatment of e.g. cancer.
CC   See also Q25113-9.
SQ   Sequence   36 BP;    4 A;    15 C;    9 G;    8 T;

  Query Match           46.2%;  Score 12;  DB 4;  Length 36;
  Best Local Similarity 100.0%;  Pred. No. 1.16e+03;
  Matches    12;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db      15 tcagccactgga 26
           ||||||||||||
Qy       4 TCAGCCACTGGA 15


RESULT   27
ID   Q11446 standard; DNA; 39 BP.
AC   Q11446;
DT   29-MAY-1991  (first entry)
DE   Probe #8 complementary to CD1a target sequence contg. AT or TA.
KW   CD1a; gene inhibition; inflammation; neoplasm; ss.
OS   Synthetic.
PN   J03007585-A.
PD   14-JAN-1991.
PF   21-SEP-1989; 410622.
PR   23-JAN-1989; US-299265.
PR   21-SEP-1989; US-410622.
PA   (UYYA-) YALE UNIV.
DR   WPI; 91-089455/13.
PT   Selective inhibition of gene manifestation - with optically active
PT   oligonucleotide reacting with target DNA to inhibit cell functions
```

```
PS   Claim 4; Page 2; 19pp; Japanese.
CC   This oligonucleotide is one of 14 that are complementary to regions
CC   of the CD1a coding sequence and have an AT or TA motif within
CC   nucleotides 12-20. The oligonucleotides are used in pharmaceutical
CC   compositions with a UVA-radiated optically active compound such as a
CC   psoralen. The UV-radiated product is able to react with target DNA
CC   under optically active conditions to inhibit cell functions.
CC   See also Q11435-Q11445 and Q11447-Q11466, Q11544-7.
SQ   Sequence   39 BP;    10 A;    10 C;    9 G;    10 T;

  Query Match          46.2%;  Score 12;  DB 2;  Length 39;
  Best Local Similarity 100.0%;  Pred. No. 1.16e+03;
  Matches    12;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db     25 cagccactggat 36
          ||||||||||||
Qy      5 CAGCCACTGGAT 16


RESULT   28
ID   Q11451 standard; DNA; 39 BP.
AC   Q11451;
DT   29-MAY-1991  (first entry)
DE   Probe #13 complementary to CD1a target sequence contg. AT or TA.
KW   CD1a; gene inhibition; inflammation; neoplasm; ss.
OS   Synthetic.
PN   J03007585-A.
PD   14-JAN-1991.
PF   21-SEP-1989; 410622.
PR   23-JAN-1989; US-299265.
PR   21-SEP-1989; US-410622.
PA   (UYYA-) YALE UNIV.
DR   WPI; 91-089455/13.
PT   Selective inhibition of gene manifestation - with optically active
PT   oligonucleotide reacting with target DNA to inhibit cell functions
PS   Claim 4; Page 2; 19pp; Japanese.
CC   This oligonucleotide is one of 14 that are complementary to regions
CC   of the CD1a coding sequence and have an AT or TA motif within
CC   nucleotides 12-20. The oligonucleotides are used in pharmaceutical
CC   compositions with a UVA-radiated optically active compound such as a
CC   psoralen. The UV-radiated product is able to react with target DNA
CC   under optically active conditions to inhibit cell functions.
CC   See also Q11435-Q11450 and Q11452-Q11466, Q11544-7.
SQ   Sequence   39 BP;    11 A;    10 C;    7 G;    11 T;

  Query Match          46.2%;  Score 12;  DB 2;  Length 39;
  Best Local Similarity 100.0%;  Pred. No. 1.16e+03;
  Matches    12;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db      8 cagccactggat 19
          ||||||||||||
Qy      5 CAGCCACTGGAT 16


RESULT   29
ID   Q49401 standard; cDNA; 46 BP.
AC   Q49401;
DT   27-APR-1994  (first entry)
DE   HIV-1 TATA region.
KW   TATA modulating factor; TMF; transcription; TATA box; promoter; HIV-1;
KW   human immunodeficiency virus-1; short arm; human chromosome 3; p12-p21;
KW   translocation; cancer; ss.
OS   Human immunodeficiency virus-1.
PN   WO9320106-A.
PD   14-OCT-1993.
PF   31-MAR-1993; U03077.
PR   02-APR-1992; US-862025.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Gaynor RB,  Wu F;
DR   WPI; 93-336836/42.
PT   New protein cellular factor - capable of binding double stranded
PT   HIV-1 tata region and activating gene expression of HIV-LTR
PS   Claim 3; Page 48; 75pp; English.
CC   This sequence represents the TATA region of the HIV-1 LTR from -46
CC   to -1.    This region is bound by TATA modulating factor (TMF).  TMF
CC   is a protein of mol. wt. 123-130 kD which activates transcription in
CC   most genes, esp. in human immunodeficiency virus-1 (HIV-1) by binding
CC   to the TATA box region of the promoter.  TMF is encoded by the short
CC   arm of human chromosome 3 in the region p12-p21 which is often
CC   involved in translocations in patients having lung and other types
CC   of cancer.
SQ   Sequence   46 BP;    8 A;    12 C;    11 G;    15 T;

  Query Match          46.2%;  Score 12;  DB 8;  Length 46;
  Best Local Similarity  77.3%;  Pred. No. 1.16e+03;
  Matches    17;  Conservative    0;  Mismatches   5;  Indels   0;  Gaps   0;

Db      7 ctcagatgctgcatataagcag 28
          |||||   ||| || |||||||
Qy      3 CTCAGCCACTGGATTTAAGCAG 24


RESULT   30
ID   T95880 standard; DNA; 49 BP.
AC   T95880;
DT   27-MAR-1998  (first entry)
DE   Competitor of 43 kDa TAR DNA binding protein (TDP-43).
KW   Tat-activation; TAR region; DNA binding protein; TDP-43;
KW   human immunodeficiency virus type-1; HIV-1; long terminal repeat;
KW   LTR; inhibition; gene expression; treatment; infection;
KW   competitor; ss.
OS   Human immunodeficiency virus type 1.
PN   US5688511-A.
PD   18-NOV-1997.
PF   22-NOV-1994; 343682.
PR   22-NOV-1994; US-343682.
PR   05-NOV-1991; US-788266.
PR   06-MAY-1994; US-239047.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Gaynor RB, Ou SI, Wu FK;
DR   WPI; 98-007932/01.
PT   Polypeptide(s) that inhibit HIV-1 gene expression - useful for
PT   treating AIDS
PS   Example 8; Columns 51-52; 31pp; English.
CC   The present sequence is a competitor of the 43 kDa
CC   Tat-activation (TAR) DNA binding protein (TDP-43), which binds a
CC   TAR region of human immunodeficiency virus type-1 (HIV-1) long
CC   terminal repeat (LTR) DNA, does not bind to TAR RNA and inhibits
CC   HIV-1 gene expression. TDP-43 can be used to treat HIV-1
CC   infections.
SQ   Sequence   49 BP;    9 A;    13 C;    12 G;    15 T;

  Query Match          46.2%;  Score 12;  DB 37;  Length 49;
  Best Local Similarity  77.3%;  Pred. No. 1.16e+03;
  Matches    17;  Conservative    0;  Mismatches   5;  Indels   0;  Gaps   0;

Db      7 ctcagatgctgcatataagcag 28
          |||||   ||| || |||||||
Qy      3 CTCAGCCACTGGATTTAAGCAG 24


Search completed: Mon Aug  2 12:34:47 1999
Job time : 155 secs.
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****

MPSRCH (TM)

****

Release 3.1A John F. Collins, Biocomputing Research Unit.

MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Mon Aug 2 12:22:01 1999; MasPar time 7.16 Seconds
257.475 Million cell updates/sec

Tabular output not generated.

Title: >US-09-121-239-27
Description: (1-26) from US09121239.seq
Perfect Score: 26
N.A. Sequence: 1 CACTCAGCCACTGGATTTAAGCAGAG 26
Comp: GTGAGTCGGTGACCTAAATTCGTCTC

Scoring table: TABLE default
Gap 10

Nmatch STD : Dbase 0; Query 0

Searched: 137068 seqs, 35432894 bases x 2

Post-processing: Minimum Match 0%
Listing first 1000 summaries
Maximum DB seq length 50

Database: n-issued
1:5A_COMB 2:5B_COMB 3:5C_COMB 4:PCT9_COMB 5:backfiles1

Statistics: Mean 5.211; Variance 2.655; scale 1.963

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
	1	21	80.8	40	3	US-08-761-	Sequence 2, Applicatio	5.79e-04
c	2	18	69.2	18	3	US-08-761-	Sequence 4, Applicatio	5.28e-02
c	3	14	53.8	18	3	US-08-761-	Sequence 5, Applicatio	1.47e+01
	4	13	50.0	18	2	US-08-363-	Sequence 9, Applicatio	5.45e+01
	5	13	50.0	22	4	PCT-US92-0	Sequence 12, Applicati	5.45e+01
	6	13	50.0	22	2	US-08-152-	Sequence 12, Applicati	5.45e+01
	7	12	46.2	20	1	US-08-259-	Sequence 46, Applicati	1.93e+02
c	8	12	46.2	21	1	US-07-665-	Sequence 47, Applicati	1.93e+02
c	9	12	46.2	21	1	US-08-106-	Sequence 47, Applicati	1.93e+02
c	10	12	46.2	23	1	US-08-399-	Sequence 98, Applicati	1.93e+02
	11	12	46.2	28	2	US-08-479-	Sequence 64, Applicati	1.93e+02
	12	12	46.2	28	2	US-08-479-	Sequence 92, Applicati	1.93e+02
c	13	12	46.2	28	2	US-08-479-	Sequence 78, Applicati	1.93e+02
c	14	12	46.2	28	2	US-08-479-	Sequence 12, Applicati	1.93e+02
	15	12	46.2	34	1	US-08-136-	Sequence 9, Applicatio	1.93e+02
	16	12	46.2	35	2	US-08-343-	Sequence 12, Applicati	1.93e+02
	17	12	46.2	36	1	US-07-794-	Sequence 23, Applicati	1.93e+02
	18	12	46.2	36	1	US-08-041-	Sequence 13, Applicati	1.93e+02
	19	12	46.2	36	1	US-08-041-	Sequence 12, Applicati	1.93e+02
	20	12	46.2	36	2	US-08-397-	Sequence 22, Applicati	1.93e+02
	21	12	46.2	36	2	US-08-397-	Sequence 23, Applicati	1.93e+02
	22	12	46.2	36	1	US-07-794-	Sequence 22, Applicati	1.93e+02
	23	12	46.2	39	5	5256648-14	Patent No. 5256648.	1.93e+02
	24	12	46.2	39	5	5256648-19	Patent No. 5256648.	1.93e+02
	25	12	46.2	39	5	5256648-13	Patent No. 5256648.	1.93e+02
	26	12	46.2	49	2	US-08-343-	Sequence 11, Applicati	1.93e+02
c	27	12	46.2	49	1	US-07-994-	Sequence 26, Applicati	1.93e+02
	28	12	46.2	50	4	PCT-US93-1	Sequence 486, Applicat	1.93e+02
	29	12	46.2	50	1	US-08-171-	Sequence 487, Applicat	1.93e+02
	30	12	46.2	50	2	US-08-123-	Sequence 487, Applicat	1.93e+02
	31	12	46.2	50	4	PCT-US93-1	Sequence 487, Applicat	1.93e+02
	32	12	46.2	50	1	US-08-171-	Sequence 486, Applicat	1.93e+02
	33	12	46.2	50	2	US-08-123-	Sequence 486, Applicat	1.93e+02
	34	11	42.3	18	3	US-08-716-	Sequence 2, Applicatio	6.47e+02
	35	11	42.3	19	3	US-08-620-	Sequence 24, Applicati	6.47e+02
	36	11	42.3	19	4	PCT-US95-0	Sequence 61, Applicati	6.47e+02
	37	11	42.3	19	2	US-08-261-	Sequence 61, Applicati	6.47e+02
	38	11	42.3	19	3	US-08-348-	Sequence 57, Applicati	6.47e+02
c	39	11	42.3	23	3	US-08-448-	Sequence 34, Applicati	6.47e+02
	40	11	42.3	28	3	US-08-078-	Sequence 17, Applicati	6.47e+02
c	41	11	42.3	30	3	US-08-468-	Sequence 13, Applicati	6.47e+02
	42	11	42.3	32	1	US-08-298-	Sequence 32, Applicati	6.47e+02
	43	11	42.3	32	1	US-08-149-	Sequence 32, Applicati	6.47e+02
c	44	11	42.3	33	3	US-08-491-	Sequence 2, Applicatio	6.47e+02
c	45	11	42.3	33	4	PCT-US94-0	Sequence 2, Applicatio	6.47e+02
	46	11	42.3	36	4	PCT-US93-0	Sequence 4, Applicatio	6.47e+02
	47	11	42.3	36	4	PCT-US93-0	Sequence 14, Applicati	6.47e+02
	48	11	42.3	36	3	US-08-162-	Sequence 14, Applicati	6.47e+02
	49	11	42.3	36	4	PCT-US95-0	Sequence 4, Applicatio	6.47e+02
	50	11	42.3	36	4	PCT-US95-0	Sequence 26, Applicati	6.47e+02
	51	11	42.3	36	4	PCT-US93-0	Sequence 23, Applicati	6.47e+02
	52	11	42.3	36	2	US-08-133-	Sequence 23, Applicati	6.47e+02
	53	11	42.3	36	2	US-08-133-	Sequence 33, Applicati	6.47e+02
	54	11	42.3	36	2	US-08-276-	Sequence 26, Applicati	6.47e+02
	55	11	42.3	36	4	PCT-US93-0	Sequence 33, Applicati	6.47e+02
	56	11	42.3	36	3	US-08-899-	Sequence 16, Applicati	6.47e+02
c	57	11	42.3	37	3	US-08-078-	Sequence 19, Applicati	6.47e+02
c	58	11	42.3	38	1	US-08-171-	Sequence 2, Applicatio	6.47e+02
	59	11	42.3	39	4	PCT-US91-0	Sequence 55, Applicati	6.47e+02
	60	11	42.3	39	2	US-08-464-	Sequence 55, Applicati	6.47e+02
c	61	11	42.3	39	2	US-08-464-	Sequence 61, Applicati	6.47e+02
c	62	11	42.3	40	3	US-08-899-	Sequence 19, Applicati	6.47e+02
c	63	11	42.3	40	3	US-08-162-	Sequence 7, Applicatio	6.47e+02
c	64	11	42.3	40	4	PCT-US93-0	Sequence 18, Applicati	6.47e+02
c	65	11	42.3	40	3	US-08-899-	Sequence 30, Applicati	6.47e+02
c	66	11	42.3	40	3	US-08-899-	Sequence 19, Applicati	6.47e+02
c	67	11	42.3	40	3	US-08-899-	Sequence 30, Applicati	6.47e+02
c	68	11	42.3	40	4	PCT-US95-0	Sequence 19, Applicati	6.47e+02
c	69	11	42.3	40	2	US-08-133-	Sequence 26, Applicati	6.47e+02
c	70	11	42.3	40	4	PCT-US93-0	Sequence 26, Applicati	6.47e+02
	71	11	42.3	42	3	US-07-853-	Sequence 106, Applicat	6.47e+02
	72	11	42.3	42	4	PCT-US92-1	Sequence 106, Applicat	6.47e+02
	73	11	42.3	42	4	PCT-US92-0	Sequence 58, Applicati	6.47e+02
	74	11	42.3	42	2	US-08-053-	Sequence 106, Applicat	6.47e+02
	75	11	42.3	47	2	US-08-303-	Sequence 60, Applicati	6.47e+02
	76	11	42.3	47	4	PCT-US95-0	Sequence 77, Applicati	6.47e+02
	77	11	42.3	50	1	US-08-171-	Sequence 587, Applicat	6.47e+02
	78	11	42.3	50	2	US-08-123-	Sequence 587, Applicat	6.47e+02
c	79	11	42.3	50	4	PCT-US93-1	Sequence 372, Applicat	6.47e+02
c	80	11	42.3	50	2	US-08-123-	Sequence 140, Applicat	6.47e+02

Note: Post-processor removed 920 summaries from list due to search parameters chosen.

ALIGNMENTS

RESULT 1
ID US-08-761-131-2 STANDARD; DNA; UNC; 40 BP.
AC xxxxxx
DT
DE Sequence 2, Application US/08761131
CC Sequence 2, Application US/08761131

```
CC   Patent No. 5804384
CC    GENERAL INFORMATION:
CC      APPLICANT:  M ller, Uwe R. et al.
CC      TITLE OF INVENTION:  DEVICES AND METHODS FOR DETECTING
CC      TITLE OF INVENTION:  MULTIPLE ANALYTES IN SAMPLES
CC      NUMBER OF SEQUENCES:  7
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Vysis, Inc.
CC        STREET:  3100 Woodcreek Drive
CC        CITY:  Downers Grove
CC        STATE:  Illinois
CC        COUNTRY:  U.S.A.
CC        ZIP:  60515
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Diskette
CC        COMPUTER:  IBM Compatible
CC        OPERATING SYSTEM:  DOS
CC        SOFTWARE:  FastSEQ Version 2.0
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/761,131
CC        FILING DATE:
CC        CLASSIFICATION:  435
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:
CC        FILING DATE:
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Galloway, No. 5804384val B.
CC        REGISTRATION NUMBER:  33,595
CC        REFERENCE/DOCKET NUMBER:  01886/064001
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  708-271-7417
CC        TELEFAX:  708-271-7048
CC        TELEX:  200154
CC     INFORMATION FOR SEQ ID NO:  2:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  40 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  single
CC        TOPOLOGY:  linear
CC      MOLECULE TYPE:  Genomic DNA
SQ   SEQUENCE 40 BP; 10 A; 10 C; 8 G; 12 T; 0 OTHER.

  Query Match           80.8%;  Score 21;  DB 3;  Length 40;
  Best Local Similarity  95.7%;  Pred. No. 5.79e-04;
  Matches    22;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db      1 ACTCAGCCACTGGATTTAAGTAG 23
          ||||||||||||||||||| ||
Qy      2 ACTCAGCCACTGGATTTAAGCAG 24


RESULT    2
ID   US-08-761-131-4 STANDARD; DNA; UNC; 18 BP.
AC   xxxxxx
DT
DE   Sequence 4, Application US/08761131
CC   Sequence 4, Application US/08761131
CC   Patent No. 5804384
CC    GENERAL INFORMATION:
CC      APPLICANT:  M ller, Uwe R. et al.
CC      TITLE OF INVENTION:  DEVICES AND METHODS FOR DETECTING
CC      TITLE OF INVENTION:  MULTIPLE ANALYTES IN SAMPLES
CC      NUMBER OF SEQUENCES:  7
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Vysis, Inc.
CC        STREET:  3100 Woodcreek Drive
CC        CITY:  Downers Grove
CC        STATE:  Illinois
CC        COUNTRY:  U.S.A.
CC        ZIP:  60515
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Diskette
CC        COMPUTER:  IBM Compatible
CC        OPERATING SYSTEM:  DOS
CC        SOFTWARE:  FastSEQ Version 2.0
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/761,131
CC        FILING DATE:
CC        CLASSIFICATION:  435
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:
CC        FILING DATE:
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Galloway, No. 5804384val B.
CC        REGISTRATION NUMBER:  33,595
CC        REFERENCE/DOCKET NUMBER:  01886/064001
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  708-271-7417
CC        TELEFAX:  708-271-7048
CC        TELEX:  200154
CC     INFORMATION FOR SEQ ID NO:  4:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  18 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  single
CC        TOPOLOGY:  linear
CC      MOLECULE TYPE:  Genomic DNA
SQ   SEQUENCE 18 BP; 5 A; 3 C; 5 G; 5 T; 0 OTHER.

  Query Match           69.2%;  Score 18;  DB 3;  Length 18;
  Best Local Similarity 100.0%;  Pred. No. 5.28e-02;
  Matches    18;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db      1 TAAATCCAGTGGCTGAGT 18
          ||||||||||||||||||
Cp     19 TAAATCCAGTGGCTGAGT 2


RESULT    3
ID   US-08-761-131-5 STANDARD; DNA; UNC; 18 BP.
AC   xxxxxx
DT
DE   Sequence 5, Application US/08761131
CC   Sequence 5, Application US/08761131
CC   Patent No. 5804384
CC    GENERAL INFORMATION:
CC      APPLICANT:  M ller, Uwe R. et al.
CC      TITLE OF INVENTION:  DEVICES AND METHODS FOR DETECTING
CC      TITLE OF INVENTION:  MULTIPLE ANALYTES IN SAMPLES
CC      NUMBER OF SEQUENCES:  7
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Vysis, Inc.
CC        STREET:  3100 Woodcreek Drive
CC        CITY:  Downers Grove
CC        STATE:  Illinois
CC        COUNTRY:  U.S.A.
CC        ZIP:  60515
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Diskette
CC        COMPUTER:  IBM Compatible
CC        OPERATING SYSTEM:  DOS
CC        SOFTWARE:  FastSEQ Version 2.0
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/761,131
CC        FILING DATE:
CC        CLASSIFICATION:  435
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:
CC        FILING DATE:
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Galloway, No. 5804384val B.
CC        REGISTRATION NUMBER:  33,595
CC        REFERENCE/DOCKET NUMBER:  01886/064001
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  708-271-7417
CC        TELEFAX:  708-271-7048
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CC         TELEX:  200154
CC     INFORMATION FOR SEQ ID NO:  5:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  18 base pairs
CC         TYPE:  nucleic acid
CC         STRANDEDNESS:  single
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  Genomic DNA
SQ   SEQUENCE 18 BP; 5 A; 3 C; 5 G; 5 T; 0 OTHER.

  Query Match           53.8%;  Score 14;  DB 3;  Length 18;
  Best Local Similarity  88.9%;  Pred. No. 1.47e+01;
  Matches    16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Db       1 TAAATGCAGTGCCTGAGT 18
           ||||| ||||| ||||||
Cp      19 TAAATCCAGTGGCTGAGT 2


RESULT    4
ID   US-08-363-233B-9 STANDARD; DNA; UNC; 18 BP.
AC   xxxxxx
DT
DE   Sequence 9, Application US/08363233B
CC   Sequence 9, Application US/08363233B
CC   Patent No. 5714383
CC    GENERAL INFORMATION:
CC      APPLICANT:  Thompson, James D.
CC      TITLE OF INVENTION:  METHOD AND REAGENT FOR TREATING CHRONIC
CC      TITLE OF INVENTION:  MYELOGENOUS LEUKEMIA
CC      NUMBER OF SEQUENCES:  39
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Lyon & Lyon
CC        STREET:  633 West Fifth Street
CC        STREET:  Suite 4700
CC        CITY:  Los Angeles
CC        STATE:  California
CC        COUNTRY:  U.S.A.
CC        ZIP:  90071-2066
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
CC        MEDIUM TYPE:  storage
CC        COMPUTER:  IBM Compatible
CC        OPERATING SYSTEM:  IBM P.C. DOS 5.0
CC        SOFTWARE:  FastSEQ for Windows 2.0
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/363,233B
CC        FILING DATE:  December 23, 1994
CC        CLASSIFICATION:  435
CC      PRIOR APPLICATION DATA:
CC      PRIOR APPLICATION DATA:  including application
CC      PRIOR APPLICATION DATA:  described below:              2
CC        APPLICATION NUMBER:  07/882,822
CC        FILING DATE:  May 14, 1992
CC        APPLICATION NUMBER:  08/193,922
CC        FILING DATE:  February 7, 1994
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Warburg, Richard J.
CC        REGISTRATION NUMBER:  32,327
CC        REFERENCE/DOCKET NUMBER:  209/165
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  (213) 489-1600
CC        TELEFAX:  (213) 955-0440
CC        TELEX:  67-3510
CC     INFORMATION FOR SEQ ID NO:  9:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  18 base pairs
CC         TYPE:  nucleic acid
CC         STRANDEDNESS:  single
CC         TOPOLOGY:  linear
SQ   SEQUENCE 18 BP; 7 A; 2 C; 4 G; 0 T; 5 OTHER.

  Query Match           50.0%;  Score 13;  DB 2;  Length 18;
  Best Local Similarity  76.9%;  Pred. No. 5.45e+01;
  Matches    10;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Db       1 GAUUUAAGCAGAG 13
           ||:::|||||||||
Qy      14 GATTTAAGCAGAG 26


RESULT    5
ID   PCT-US92-05035-12 STANDARD; DNA; UNC; 22 BP.
AC   xxxxxx
DT
DE   Sequence 12, Application PC/TUS9205035
CC   Sequence 12, Application PC/TUS9205035
CC    GENERAL INFORMATION:
CC      APPLICANT:  Calabretta, Bruno
CC      APPLICANT:  Gewirtz, Alan M.
CC      TITLE OF INVENTION:  Selective Inhibition of
CC      TITLE OF INVENTION:  Leukemic Cell Proliferation by bcr-abl
CC      TITLE OF INVENTION:  Antisense Oligonucleotides
CC      NUMBER OF SEQUENCES:  34
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Temple University - Of The Common-
CC        ADDRESSEE:  wealth System of Higher Education
CC        STREET:  406 University Services Building
CC        CITY:  Philadelphia
CC        STATE:  Pennsylvania
CC        COUNTRY:  U.S.A.
CC        ZIP:  19122
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Diskette, 3.50 inch, 720 Kb
CC        COMPUTER:  IBM PS/2
CC        OPERATING SYSTEM:  MS-DOS
CC        SOFTWARE:  WordPerfect 5.1
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  PCT/US92/05035
CC        FILING DATE:  19920615
CC        CLASSIFICATION:  514
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  07/718,302
CC        FILING DATE:  June 18, 1991
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  07/869,911
CC        FILING DATE:  April 14, 1991
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Monaco, Daniel A.
CC        REGISTRATION NUMBER:  30,480
CC        REFERENCE/DOCKET NUMBER:  6056-120 (CIP) 1
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  (215) 568-8383
CC        TELEFAX:  (215) 568-5549
CC        TELEX:  None
CC     INFORMATION FOR SEQ ID NO:  12:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  22 Nucleotides
CC         TYPE:  NUCLEIC ACID
CC         STRANDEDNESS:  single stranded
CC         TOPOLOGY:  not relevant
SQ   SEQUENCE 22 BP; 4 A; 9 C; 4 G; 5 T; 0 OTHER.

  Query Match           50.0%;  Score 13;  DB 4;  Length 22;
  Best Local Similarity 100.0%;  Pred. No. 5.45e+01;
  Matches    13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Db      10 CACTCAGCCACTG 22
           |||||||||||||
Qy       1 CACTCAGCCACTG 13


RESULT    6
ID   US-08-152-621-12 STANDARD; DNA; UNC; 22 BP.
AC   xxxxxx
DT
```

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DE   Sequence 12, Application US/08152621
CC   Sequence 12, Application US/08152621
CC   Patent No. 5652222
CC    GENERAL INFORMATION:
CC      APPLICANT:  Calabretta, Bruno
CC      APPLICANT:  Gewirtz, Alan M.
CC      TITLE OF INVENTION:  Selective Inhibition of
CC      TITLE OF INVENTION:  Leukemic Cell Proliferation by bcr-abl
CC      TITLE OF INVENTION:  Antisense Oligonucleotides
CC      NUMBER OF SEQUENCES:  34
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  SEIDEL, GONDA, LAVORGNA
CC        ADDRESSEE:  & MONACO, P.C.
CC        STREET:  1800 Two Penn Center
CC        CITY:  Philadelphia
CC        STATE:  Pennsylvania
CC        COUNTRY:  U.S.A.
CC        ZIP:  19102
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Diskette, 3.50 inch, 720 Kb
CC        COMPUTER:  IBM PS/2
CC        OPERATING SYSTEM:  MS-DOS
CC        SOFTWARE:  WordPerfect 5.1
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/152,621
CC        FILING DATE:  No. 5652222ember 15, 1993.
CC        CLASSIFICATION:  514
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  07/718,302
CC        FILING DATE:  June 18, 1991
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Monaco, Daniel A.
CC        REGISTRATION NUMBER:  30,480
CC        REFERENCE/DOCKET NUMBER:  6056-120 (CT.) 1
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  (215) 568-8383
CC        TELEFAX:  (215) 568-5549
CC        TELEX:  No. 5652222e
CC    INFORMATION FOR SEQ ID NO:  12:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  22 Nucleotides
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  single stranded
CC        TOPOLOGY:  not relevant
SQ   SEQUENCE 22 BP; 4 A; 9 C; 4 G; 5 T; 0 OTHER.

  Query Match           50.0%;  Score 13;  DB 2;  Length 22;
  Best Local Similarity 100.0%;  Pred. No. 5.45e+01;
  Matches   13;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Db     10 CACTCAGCCACTG 22
           |||||||||||||
Qy      1 CACTCAGCCACTG 13


RESULT    7
ID   US-08-259-745A-46 STANDARD; DNA; UNC; 20 BP.
AC   xxxxxx
DT
DE   Sequence 46, Application US/08259745A
CC   Sequence 46, Application US/08259745A
CC   Patent No. 5582983
CC    GENERAL INFORMATION:
CC      APPLICANT:  Anderson, Donald
CC      APPLICANT:  Scholin, Christoper
CC      TITLE OF INVENTION:  GENETIC MARKERS AND METHODS OF IDENTIFYING ALEXANDRIUM
CC      NUMBER OF SEQUENCES:  49
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  DIKE, BRONSTEIN, ROBERTS & CUSHMAN
CC        STREET:  130 Water Street
CC        CITY:  Boston
CC        STATE:  MA
CC        COUNTRY:  U.S.A.
CC        ZIP:  02109
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Diskette
CC        COMPUTER:  IBM Compatible
CC        OPERATING SYSTEM:  DOS
CC        SOFTWARE:  FastSEQ Version 1.5
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/259,745A
CC        FILING DATE:  14-JUN-1994
CC        CLASSIFICATION:  435
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  07/967,637
CC        FILING DATE:  28-OCT-1992
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Neuner, George W
CC        REGISTRATION NUMBER:  26,964
CC        REFERENCE/DOCKET NUMBER:  42,101 FWC
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  617-523-3400
CC        TELEFAX:  617-523-6440
CC        TELEX:
CC    INFORMATION FOR SEQ ID NO:  46:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  20 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  single
CC        TOPOLOGY:  linear
CC      MOLECULE TYPE:  preRNA
CC      HYPOTHETICAL:  NO
CC      ANTI-SENSE:  NO
CC      FRAGMENT TYPE:
CC      ORIGINAL SOURCE:
SQ   SEQUENCE 20 BP; 7 A; 5 C; 3 G; 5 T; 0 OTHER.

  Query Match           46.2%;  Score 12;  DB 1;  Length 20;
  Best Local Similarity 87.5%;  Pred. No. 1.93e+02;
  Matches   14;  Conservative   0;  Mismatches   2;  Indels   0;  Gaps   0;

Db      3 CCGCTGAATTTAAGCA 18
            || ||| |||||||||
Qy      8 CCACTGGATTTAAGCA 23


RESULT    8
ID   US-07-665-960A-47 STANDARD; DNA; UNC; 21 BP.
AC   xxxxxx
DT
DE   Sequence 47, Application US/07665960A
CC   Sequence 47, Application US/07665960A
CC   Patent No. 5578443
CC    GENERAL INFORMATION:
CC      APPLICANT:  Santamaria, Pedro
CC      APPLICANT:  Boyce-Jacino, Michael T.
CC      APPLICANT:  Barbosa, Jose J.
CC      APPLICANT:  Rich, Stephen S.
CC      APPLICANT:  Faras, Anthony J.
CC      TITLE OF INVENTION:  DNA Sequence-Based HLA Typing
CC      TITLE OF INVENTION:  Method
CC      NUMBER OF SEQUENCES:  49
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Merchant & Gould
CC        STREET:  3100 No. 5578443west Center
CC        CITY:  Minneapolis
CC        STATE:  Minnesota
CC        COUNTRY:  USA
CC        ZIP:  55402
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Diskette, 3.5 inch, 720 Kb.
CC        COMPUTER:  No. 5578443thgate 386
CC        OPERATING SYSTEM:  DOS 4.0
CC        SOFTWARE:  WordPerfect~ 5.0
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/07/665,960A
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CC        FILING DATE:  19910306
CC        CLASSIFICATION:  435
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Kowalchyk, Alan W.
CC        REGISTRATION NUMBER:  31,535
CC        REFERENCE/DOCKET NUMBER:  600.190-US-01
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  (612) 332-5300
CC        TELEFAX:  (612) 332-9081
CC    INFORMATION FOR SEQ ID NO:  47:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  21 base pairs
CC        TYPE:  NUCLEIC ACID
CC        STRANDEDNESS:  Single
CC        TOPOLOGY:  Linear
CC      MOLECULE TYPE:  Genomic DNA
CC      ANTI-SENSE:  no
CC      FRAGMENT TYPE:  Internal Fragment
CC      ORIGINAL SOURCE:  Synthetically Derived
CC      FEATURE:
CC        NAME/KEY:  Oligonucleotide Primer DQB6
CC        LOCATION:  Anneals to codons -8 to -2 of the
CC        LOCATION:  DQB1 transcript of HLA class II
SQ   SEQUENCE 21 BP; 4 A; 7 C; 7 G; 3 T; 0 OTHER.

  Query Match           46.2%;  Score 12;  DB 1;  Length 21;
  Best Local Similarity 100.0%;  Pred. No. 1.93e+02;
  Matches   12;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db      10 CCAGTGGCTGAG 21
           ||||||||||||
Cp      14 CCAGTGGCTGAG 3


RESULT    9
ID   US-08-106-802-47 STANDARD; DNA; UNC; 21 BP.
AC   xxxxxx
DT
DE   Sequence 47, Application US/08106802
CC   Sequence 47, Application US/08106802
CC   Patent No. 5629149
CC    GENERAL INFORMATION:
CC      APPLICANT:  Santamaria, Pedro
CC      APPLICANT:  Boyce-Jacino, Michael T.
CC      APPLICANT:  Barbosa, Jose J.
CC      APPLICANT:  Rich, Stephen S.
CC      APPLICANT:  Faras, Anthony J.
CC      TITLE OF INVENTION:  DNA Sequence-Based HLA Typing
CC      TITLE OF INVENTION:  Method
CC      NUMBER OF SEQUENCES:  49
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Merchant & Gould
CC        STREET:  3100 No. 5629149west Center
CC        CITY:  Minneapolis
CC        STATE:  Minnesota
CC        COUNTRY:  USA
CC        ZIP:  55402
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Diskette, 3.5 inch, 720 Kb.
CC        COMPUTER:  PC/XT/AT or compatible
CC        OPERATING SYSTEM:  MS-DOS 3.30
CC        SOFTWARE:  ASCII
CC        SOFTWARE:  (Origin: WordPerfect  5.0)
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/106,802
CC        FILING DATE:  16-AUG-1993
CC        CLASSIFICATION:  435
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  07/833,668
CC        FILING DATE:  18-FEB-1992
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Kowalchyk, Alan W.
CC        REGISTRATION NUMBER:  31,535
CC        REFERENCE/DOCKET NUMBER:  600.243-US-01
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  (612) 332-5300
CC        TELEFAX:  (612) 332-9081
CC    INFORMATION FOR SEQ ID NO:  47:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  21 base pairs
CC        TYPE:  Nucleic Acid
CC        STRANDEDNESS:  Single
CC        TOPOLOGY:  Linear
CC      MOLECULE TYPE:  Genomic DNA
CC      ANTI-SENSE:  no
CC      FRAGMENT TYPE:  Internal Fragment
CC      ORIGINAL SOURCE:  Synthetically Derived
CC      FEATURE:
CC        NAME/KEY:  Oligonucleotide Primer DQB6
CC        LOCATION:  Anneals to codons -8 to -2 of the
CC        LOCATION:  DQB1 transcript of HLA class II
SQ   SEQUENCE 21 BP; 4 A; 7 C; 7 G; 3 T; 0 OTHER.

  Query Match           46.2%;  Score 12;  DB 1;  Length 21;
  Best Local Similarity 100.0%;  Pred. No. 1.93e+02;
  Matches   12;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db      10 CCAGTGGCTGAG 21
           ||||||||||||
Cp      14 CCAGTGGCTGAG 3


RESULT   10
ID   US-08-399-412A-98 STANDARD; DNA; UNC; 23 BP.
AC   xxxxxx
DT
DE   Sequence 98, Application US/08399412A
CC   Sequence 98, Application US/08399412A
CC   Patent No. 5622828
CC    GENERAL INFORMATION:
CC      APPLICANT:  Parma, David
CC      APPLICANT:  Gold, Larry
CC      TITLE OF INVENTION:  High-Affinity Oligonucleotide
CC      TITLE OF INVENTION:  Ligands To Secretory Phospholipase
CC      TITLE OF INVENTION:  A2 (sPLA2)
CC      NUMBER OF SEQUENCES:  122
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Swanson & Bratschun, L.L.C.
CC        STREET:  8400 E. Prentice Avenue, Suite 200
CC        CITY:  Englewood
CC        STATE:  Colorado
CC        COUNTRY:  USA
CC        ZIP:  80111
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Diskette, 3.5 inch, 1.44 MB storage
CC        COMPUTER:  IBM compatible
CC        OPERATING SYSTEM:  MS-DOS
CC        SOFTWARE:  WordPerfect 5.1
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/399,412A
CC        FILING DATE:  6-MARCH-1995
CC        CLASSIFICATION:  536
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  07/714,131
CC        FILING DATE:  10-JUNE-1991
CC        CLASSIFICATION:  536
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  07/536,428
CC        FILING DATE:  11-JUNE-1990
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  07/964,624
CC        FILING DATE:  21-OCTOBER-1992
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Julie L. Bernard
CC        REGISTRATION NUMBER:  36,450
CC        REFERENCE/DOCKET NUMBER:  NEX27
```

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CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  (303) 793-3333
CC        TELEFAX:  (303) 793-3433
CC    INFORMATION FOR SEQ ID NO:  98:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  23 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  single
CC        TOPOLOGY:  linear
SQ   SEQUENCE 23 BP; 3 A; 5 C; 4 G; 0 T; 11 OTHER.

  Query Match           46.2%;  Score 12;  DB 1;  Length 23;
  Best Local Similarity  25.0%;  Pred. No. 1.93e+02;
  Matches    4;  Conservative   10;  Mismatches   2;  Indels   0;  Gaps   0;

Db      1 CUCWRCUUACRGBYMV 16
          |:|::|::| : ::::
Cp     26 CTCTGCTTAAATCCAG 11


RESULT   11
ID   US-08-479-852-64 STANDARD; DNA; UNC; 28 BP.
AC   xxxxxx
DT
DE   Sequence 64, Application US/08479852
CC   Sequence 64, Application US/08479852
CC   Patent No. 5712385
CC    GENERAL INFORMATION:
CC      APPLICANT:  Sherrol H. McDonough, Thomas B. Ryder,
CC      APPLICANT:  Yeasing Yang
CC      TITLE OF INVENTION:  NUCLEIC ACID AMPLIFICATION
CC      TITLE OF INVENTION:  OLIGONUCLEOTIDES AND PROBES
CC      TITLE OF INVENTION:  TO HUMAN IMMUNODEFICIENCY VIRUS TYPE 1
CC      NUMBER OF SEQUENCES:  139
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Lyon & Lyon
CC        STREET:  611 West Sixth Street
CC        CITY:  Los Angeles
CC        STATE:  California
CC        COUNTRY:  USA
CC        ZIP:  90017
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  3.5" Diskette, 1.44 Mb storage
CC        COMPUTER:  IBM PS/2 Model 50Z or 55SX
CC        OPERATING SYSTEM:  IBM P.C. DOS (Version 3.30)
CC        SOFTWARE:  WordPerfect (Version 5.0)
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/479,852
CC        FILING DATE:
CC        CLASSIFICATION:  435
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/040,745
CC        FILING DATE:
CC        APPLICATION NUMBER:  U.S. Serial No. 5712385 07/550,837
CC        FILING DATE:  7/10/90
CC        APPLICATION NUMBER:  U.S. Serial No. 5712385 07/379,501
CC        FILING DATE:  7/11/89
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Warburg, Richard J.
CC        REGISTRATION NUMBER:  32,327
CC        REFERENCE/DOCKET NUMBER:  196/189
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  (213) 489-1600
CC        TELEFAX:  (213) 955-0440
CC        TELEX:  67-3510
CC    INFORMATION FOR SEQ ID NO:  64:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  28
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  single
CC        TOPOLOGY:  linear
SQ   SEQUENCE 28 BP; 7 A; 10 C; 5 G; 6 T; 0 OTHER.

  Query Match           46.2%;  Score 12;  DB 2;  Length 28;
  Best Local Similarity  77.3%;  Pred. No. 1.93e+02;
  Matches   17;  Conservative    0;  Mismatches   5;  Indels   0;  Gaps   0;

Db      3 CTCAGATCCTGCATATAAGCAG 24
          |||||   ||| || |||||||
Qy      3 CTCAGCCACTCGATTTAAGCAG 24


RESULT   12
ID   US-08-479-852-92 STANDARD; DNA; UNC; 28 BP.
AC   xxxxxx
DT
DE   Sequence 92, Application US/08479852
CC   Sequence 92, Application US/08479852
CC   Patent No. 5712385
CC    GENERAL INFORMATION:
CC      APPLICANT:  Sherrol H. McDonough, Thomas B. Ryder,
CC      APPLICANT:  Yeasing Yang
CC      TITLE OF INVENTION:  NUCLEIC ACID AMPLIFICATION
CC      TITLE OF INVENTION:  OLIGONUCLEOTIDES AND PROBES
CC      TITLE OF INVENTION:  TO HUMAN IMMUNODEFICIENCY VIRUS TYPE 1
CC      NUMBER OF SEQUENCES:  139
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Lyon & Lyon
CC        STREET:  611 West Sixth Street
CC        CITY:  Los Angeles
CC        STATE:  California
CC        COUNTRY:  USA
CC        ZIP:  90017
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  3.5" Diskette, 1.44 Mb storage
CC        COMPUTER:  IBM PS/2 Model 50Z or 55SX
CC        OPERATING SYSTEM:  IBM P.C. DOS (Version 3.30)
CC        SOFTWARE:  WordPerfect (Version 5.0)
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/479,852
CC        FILING DATE:
CC        CLASSIFICATION:  435
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/040,745
CC        FILING DATE:
CC        APPLICATION NUMBER:  U.S. Serial No. 5712385 07/550,837
CC        FILING DATE:  7/10/90
CC        APPLICATION NUMBER:  U.S. Serial No. 5712385 07/379,501
CC        FILING DATE:  7/11/89
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Warburg, Richard J.
CC        REGISTRATION NUMBER:  32,327
CC        REFERENCE/DOCKET NUMBER:  196/189
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  (213) 489-1600
CC        TELEFAX:  (213) 955-0440
CC        TELEX:  67-3510
CC    INFORMATION FOR SEQ ID NO:  92:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  28
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  single
CC        TOPOLOGY:  linear
SQ   SEQUENCE 28 BP; 7 A; 10 C; 5 G; 0 T; 6 OTHER.

  Query Match           46.2%;  Score 12;  DB 2;  Length 28;
  Best Local Similarity  59.1%;  Pred. No. 1.93e+02;
  Matches   13;  Conservative    4;  Mismatches   5;  Indels   0;  Gaps   0;

Db      3 CUCAGAUCCUGCAUAUAAGCAG 24
          |:|||   |:| |: :||||||
Qy      3 CTCAGCCACTCGATTTAAGCAG 24


RESULT   13
ID   US-08-479-852-78 STANDARD; DNA; UNC; 28 BP.
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```
AC   xxxxxx
DT
DE   Sequence 78, Application US/08479852
CC   Sequence 78, Application US/08479852
CC   Patent No. 5712385
CC    GENERAL INFORMATION:
CC      APPLICANT:  Sherrol H. McDonough, Thomas B. Ryder,
CC      APPLICANT:  Yeasing Yang
CC      TITLE OF INVENTION:  NUCLEIC ACID AMPLIFICATION
CC      TITLE OF INVENTION:  OLIGONUCLEOTIDES AND PROBES
CC      TITLE OF INVENTION:  TO HUMAN IMMUNODEFICIENCY VIRUS TYPE 1
CC      NUMBER OF SEQUENCES:  139
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Lyon & Lyon
CC        STREET:  611 West Sixth Street
CC        CITY:  Los Angeles
CC        STATE:  California
CC        COUNTRY:  USA
CC        ZIP:  90017
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  3.5" Diskette, 1.44 Mb storage
CC        COMPUTER:  IBM PS/2 Model 50Z or 55SX
CC        OPERATING SYSTEM:  IBM P.C. DOS (Version 3.30)
CC        SOFTWARE:  WordPerfect (Version 5.0)
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/479,852
CC        FILING DATE:
CC        CLASSIFICATION:  435
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/040,745
CC        FILING DATE:
CC        APPLICATION NUMBER:  U.S. Serial No. 5712385 07/550,837
CC        FILING DATE:  7/10/90
CC        APPLICATION NUMBER:  U.S. Serial No. 5712385 07/379,501
CC        FILING DATE:  7/11/89
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Warburg, Richard J.
CC        REGISTRATION NUMBER:  32,327
CC        REFERENCE/DOCKET NUMBER:  196/189
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  (213) 489-1600
CC        TELEFAX:  (213) 955-0440
CC        TELEX:  67-3510
CC    INFORMATION FOR SEQ ID NO:  78:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  28
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  single
CC        TOPOLOGY:  linear
SQ   SEQUENCE 28 BP; 6 A; 5 C; 10 G; 0 T; 7 OTHER.

  Query Match           46.2%;  Score 12;  DB 2;  Length 28;
  Best Local Similarity  54.5%;  Pred. No. 1.93e+02;
  Matches   12;  Conservative    5;  Mismatches   5;  Indels   0;  Gaps   0;

Db       5 CUGCUUAUAUGCAGGAUCUGAG 26
           |:||::| |: |||   |:|||
Cp      24 CTGCTTAAATCCAGTGGCTGAG 3


RESULT   14
ID   US-08-479-852-12 STANDARD; DNA; UNC; 28 BP.
AC   xxxxxx
DT
DE   Sequence 12, Application US/08479852
CC   Sequence 12, Application US/08479852
CC   Patent No. 5712385
CC    GENERAL INFORMATION:
CC      APPLICANT:  Sherrol H. McDonough, Thomas B. Ryder,
CC      APPLICANT:  Yeasing Yang
CC      TITLE OF INVENTION:  NUCLEIC ACID AMPLIFICATION
CC      TITLE OF INVENTION:  OLIGONUCLEOTIDES AND PROBES
CC      TITLE OF INVENTION:  TO HUMAN IMMUNODEFICIENCY VIRUS TYPE 1
CC      NUMBER OF SEQUENCES:  139
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Lyon & Lyon
CC        STREET:  611 West Sixth Street
CC        CITY:  Los Angeles
CC        STATE:  California
CC        COUNTRY:  USA
CC        ZIP:  90017
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  3.5" Diskette, 1.44 Mb storage
CC        COMPUTER:  IBM PS/2 Model 50Z or 55SX
CC        OPERATING SYSTEM:  IBM P.C. DOS (Version 3.30)
CC        SOFTWARE:  WordPerfect (Version 5.0)
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/479,852
CC        FILING DATE:
CC        CLASSIFICATION:  435
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/040,745
CC        FILING DATE:
CC        APPLICATION NUMBER:  U.S. Serial No. 5712385 07/550,837
CC        FILING DATE:  7/10/90
CC        APPLICATION NUMBER:  U.S. Serial No. 5712385 07/379,501
CC        FILING DATE:  7/11/89
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Warburg, Richard J.
CC        REGISTRATION NUMBER:  32,327
CC        REFERENCE/DOCKET NUMBER:  196/189
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  (213) 489-1600
CC        TELEFAX:  (213) 955-0440
CC        TELEX:  67-3510
CC    INFORMATION FOR SEQ ID NO:  12:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  28
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  single
CC        TOPOLOGY:  linear
SQ   SEQUENCE 28 BP; 6 A; 5 C; 10 G; 7 T; 0 OTHER.

  Query Match           46.2%;  Score 12;  DB 2;  Length 28;
  Best Local Similarity  77.3%;  Pred. No. 1.93e+02;
  Matches   17;  Conservative    0;  Mismatches   5;  Indels   0;  Gaps   0;

Db       5 CTGCTTATATGCAGGATCTGAG 26
           ||||||| || |||   |||||
Cp      24 CTGCTTAAATCCAGTGGCTGAG 3


RESULT   15
ID   US-08-136-119-9 STANDARD; DNA; UNC; 34 BP.
AC   xxxxxx
DT
DE   Sequence 9, Application US/08136119
CC   Sequence 9, Application US/08136119
CC   Patent No. 5473056
CC    GENERAL INFORMATION:
CC      APPLICANT:  Heimbrook, David C.
CC      APPLICANT:  Hoyle, Mona I.
CC      APPLICANT:  Oliff, Allen I.
CC      TITLE OF INVENTION:  E 2F-2, A NOVEL MAMMALIAN TRANSCRIPTION
CC      TITLE OF INVENTION:  FACTOR
CC      NUMBER OF SEQUENCES:  29
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  David A. Muthard
CC        STREET:  P.O. Box 2000, 126 Lincoln Avenue
CC        CITY:  Rahway
CC        STATE:  N.J
CC        COUNTRY:  USA
CC        ZIP:  07065-0907
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
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CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, Version #1.25
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/136,119
CC        FILING DATE:
CC        CLASSIFICATION:  435
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Muthard, David A.
CC        REGISTRATION NUMBER:  35,297
CC        REFERENCE/DOCKET NUMBER:  19042
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  (908)594-3903
CC        TELEFAX:  (908)594-4720
CC    INFORMATION FOR SEQ ID NO:  9:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  34 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  single
CC        TOPOLOGY:  linear
CC      MOLECULE TYPE:  cDNA
SQ   SEQUENCE 34 BP; 6 A; 7 C; 11 G; 10 T; 0 OTHER.

  Query Match           46.2%;  Score 12;  DB 1;  Length 34;
  Best Local Similarity 100.0%;  Pred. No. 1.93e+02;
  Matches    12;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db     12 CAGCCACTGGAT 23
           ||||||||||||
Qy      5 CAGCCACTGGAT 16


RESULT   16
ID   US-08-343-682-12 STANDARD; DNA; UNC; 35 BP.
AC   xxxxxx
DT
DE   Sequence 12, Application US/08343682
CC   Sequence 12, Application US/08343682
CC   Patent No. 5688511
CC    GENERAL INFORMATION:
CC      APPLICANT:  Gaynor, Richard B.
CC      APPLICANT:  Ou, S.-H. I.
CC      APPLICANT:  Wu, Foon K.
CC      TITLE OF INVENTION:  Cellular Protein TDP-43 and Regulation
CC      TITLE OF INVENTION:  of HIV-1 Gene Expression
CC      NUMBER OF SEQUENCES:  17
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Arnold, White & Durkee
CC        STREET:  P.O. Box 4433
CC        CITY:  Houston
CC        STATE:  TX
CC        COUNTRY:  US
CC        ZIP:  77210
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, Version #1.25
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/343,682
CC        FILING DATE:  22-NOV-1994
CC        CLASSIFICATION:  435
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Mayfield, Denise L.
CC        REGISTRATION NUMBER:  33,732
CC        REFERENCE/DOCKET NUMBER:  UTSD:355/MAY
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  713/787-1400
CC        TELEFAX:  713/789-2679
CC        TELEX:  N/A
CC    INFORMATION FOR SEQ ID NO:  12:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  35 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  single
CC        TOPOLOGY:  linear
CC      MOLECULE TYPE:  DNA (genomic)
SQ   SEQUENCE 35 BP; 7 A; 9 C; 9 G; 10 T; 0 OTHER.

  Query Match           46.2%;  Score 12;  DB 2;  Length 35;
  Best Local Similarity 77.3%;  Pred. No. 1.93e+02;
  Matches    17;  Conservative    0;  Mismatches   5;  Indels   0;  Gaps   0;

Db      7 CTCAGATGCTGCATATAAGCAG 28
          |||||   ||| || |||||||
Qy      3 CTCAGCCACTGGATTTAAGCAG 24


RESULT   17
ID   US-07-794-400-23 STANDARD; DNA; UNC; 36 BP.
AC   xxxxxx
DT
DE   Sequence 23, Application US/07794400
CC   Sequence 23, Application US/07794400
CC   Patent No. 5422104
CC    GENERAL INFORMATION:
CC      APPLICANT:  Fiers, W.
CC      APPLICANT:  Tavernier, J.
CC      APPLICANT:  Van Ostade, X.
CC      TITLE OF INVENTION:  TNF-Muteins
CC      NUMBER OF SEQUENCES:  24
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Hoffmann-La Roche Inc.
CC        STREET:  340 Kingsland Street
CC        CITY:  Nutley
CC        STATE:  New Jersey
CC        COUNTRY:  USA
CC        ZIP:  07110
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, Version #1.25
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/07/794,400
CC        FILING DATE:  19911120
CC        CLASSIFICATION:  435
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  EP 90810901.0
CC        FILING DATE:  21-NOV-1990
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Krovatin, William
CC        REGISTRATION NUMBER:  33256
CC        REFERENCE/DOCKET NUMBER:  4105/136-00
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  (201) 235-4387
CC        TELEFAX:  (201) 235-3500
CC    INFORMATION FOR SEQ ID NO:  23:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  36 base pairs
CC        TYPE:  NUCLEIC ACID
CC        STRANDEDNESS:  single
CC        TOPOLOGY:  linear
CC      MOLECULE TYPE:  DNA (oligonucleotide)
CC      FEATURE:
CC        NAME/KEY:  misc_feature
CC        LOCATION:  1..36
CC        OTHER INFORMATION:  /function= "PCR primer for
CC        OTHER INFORMATION:  mutagenesis"
CC        OTHER INFORMATION:  /note= "PCR primer for mutagenesis which is
CC        OTHER INFORMATION:  complementary to positions 219-184 of Seq. ID No. 54221
CC        OTHER INFORMATION:  2 with mismatched bases at positions 7-9 and 11-12
SQ   SEQUENCE 36 BP; 5 A; 11 C; 10 G; 10 T; 0 OTHER.

  Query Match           46.2%;  Score 12;  DB 1;  Length 36;
  Best Local Similarity 100.0%;  Pred. No. 1.93e+02;
  Matches    12;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;
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Db      15 TCAGCCACTGGA 26
           ||||||||||||
Qy       4 TCAGCCACTGGA 15


RESULT   18
ID   US-08-041-648-13 STANDARD; DNA; UNC; 36 BP.
AC   xxxxxx
DT
DE   Sequence 13, Application US/08041648
CC   Sequence 13, Application US/08041648
CC   Patent No. 5486463
CC    GENERAL INFORMATION:
CC      APPLICANT:  Lesslauer, Werner
CC      APPLICANT:  L tscher, Hansruedi
CC      APPLICANT:  St ber, Dietrich
CC      TITLE OF INVENTION:  TNF-MUTEINS
CC      NUMBER OF SEQUENCES:  17
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  George M. Gould, Esq., Hoffmann-La Roche Inc.
CC        STREET:  340 Kingsland Street
CC        CITY:  Nutley
CC        STATE:  New Jersey
CC        COUNTRY:  U.S.A.
CC        ZIP:  07110-1199
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, Version #1.25
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/041,648
CC        FILING DATE:  1-APR-1993
CC        CLASSIFICATION:  435
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  EP 92810249.0
CC        FILING DATE:  2-APR-1992
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Roseman, Catherine R.
CC        REGISTRATION NUMBER:  34240
CC        REFERENCE/DOCKET NUMBER:  RAN 4105/147
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  (201) 235-6208
CC        TELEFAX:  (201) 235-3500
CC    INFORMATION FOR SEQ ID NO:  13:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  36 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  single
CC        TOPOLOGY:  linear
CC      MOLECULE TYPE:  DNA (genomic)
CC      HYPOTHETICAL:  NO
CC      ANTI-SENSE:  NO
CC      ORIGINAL SOURCE:
CC        ORGANISM:  Primer 21/M6
SQ   SEQUENCE 36 BP; 5 A; 11 C; 10 G; 10 T; 0 OTHER.

  Query Match           46.2%;  Score 12;  DB 1;  Length 36;
  Best Local Similarity 100.0%;  Pred. No. 1.93e+02;
  Matches    12;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db      15 TCAGCCACTGGA 26
           ||||||||||||
Qy       4 TCAGCCACTGGA 15


RESULT   19
ID   US-08-041-648-12 STANDARD; DNA; UNC; 36 BP.
AC   xxxxxx
DT
DE   Sequence 12, Application US/08041648
CC   Sequence 12, Application US/08041648
CC   Patent No. 5486463
CC    GENERAL INFORMATION:
CC      APPLICANT:  Lesslauer, Werner
CC      APPLICANT:  L tscher, Hansruedi
CC      APPLICANT:  St ber, Dietrich
CC      TITLE OF INVENTION:  TNF-MUTEINS
CC      NUMBER OF SEQUENCES:  17
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  George M. Gould, Esq., Hoffmann-La Roche Inc.
CC        STREET:  340 Kingsland Street
CC        CITY:  Nutley
CC        STATE:  New Jersey
CC        COUNTRY:  U.S.A.
CC        ZIP:  07110-1199
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, Version #1.25
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/041,648
CC        FILING DATE:  1-APR-1993
CC        CLASSIFICATION:  435
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  EP 92810249.0
CC        FILING DATE:  2-APR-1992
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Roseman, Catherine R.
CC        REGISTRATION NUMBER:  34240
CC        REFERENCE/DOCKET NUMBER:  RAN 4105/147
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  (201) 235-6208
CC        TELEFAX:  (201) 235-3500
CC    INFORMATION FOR SEQ ID NO:  12:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  36 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  single
CC        TOPOLOGY:  linear
CC      MOLECULE TYPE:  DNA (genomic)
CC      HYPOTHETICAL:  NO
CC      ANTI-SENSE:  NO
CC      ORIGINAL SOURCE:
CC        ORGANISM:  Primer 21/M5
SQ   SEQUENCE 36 BP; 4 A; 15 C; 9 G; 8 T; 0 OTHER.

  Query Match           46.2%;  Score 12;  DB 1;  Length 36;
  Best Local Similarity 100.0%;  Pred. No. 1.93e+02;
  Matches    12;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db      15 TCAGCCACTGGA 26
           ||||||||||||
Qy       4 TCAGCCACTGGA 15


RESULT   20
ID   US-08-397-470-22 STANDARD; DNA; UNC; 36 BP.
AC   xxxxxx
DT
DE   Sequence 22, Application US/08397470
CC   Sequence 22, Application US/08397470
CC   Patent No. 5652353
CC    GENERAL INFORMATION:
CC      APPLICANT:  Fiers, W.
CC      APPLICANT:  Tavernier, J.
CC      APPLICANT:  Van Ostade, X.
CC      TITLE OF INVENTION:  TNF-Muteins
CC      NUMBER OF SEQUENCES:  24
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Hoffmann-La Roche Inc.
CC        STREET:  340 Kingsland Street
CC        CITY:  Nutley
CC        STATE:  New Jersey
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CC         COUNTRY:  USA
CC         ZIP:  07110
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, Version #1.25
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/397,470
CC         FILING DATE:  01-MAR-1995
CC         CLASSIFICATION:  435
CC       PRIOR APPLICATION DATA:
CC         APPLICATION NUMBER:  US 07/794,400
CC         FILING DATE:  20-NOV-1991
CC         APPLICATION NUMBER:  EP 90810901.0
CC         FILING DATE:  21-NOV-1990
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Krovatin, William
CC         REGISTRATION NUMBER:  33256
CC         REFERENCE/DOCKET NUMBER:  4105/136-00
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  (201) 235-4387
CC         TELEFAX:  (201) 235-3500
CC     INFORMATION FOR SEQ ID NO:  22:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  36 base pairs
CC         TYPE:  nucleic acid
CC         STRANDEDNESS:  single
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  DNA (oligonucleotide)
CC       FEATURE:
CC         NAME/KEY:  misc_feature
CC         LOCATION:  1..36
CC         OTHER INFORMATION:  /function= "PCR primer"
CC         OTHER INFORMATION:  /product= "primer 21/M5"
CC         OTHER INFORMATION:  /note= "PCR primer which is complementary to
CC         OTHER INFORMATION:  positions 219-184 of Seq. ID No. 5652353 2 with mismatched
CC         OTHER INFORMATION:  residues at positions 10-12."
SQ   SEQUENCE 36 BP; 4 A; 15 C; 9 G; 8 T; 0 OTHER.

  Query Match           46.2%;  Score 12;  DB 2;  Length 36;
  Best Local Similarity 100.0%;  Pred. No. 1.93e+02;
  Matches    12;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db      15 TCAGCCACTGGA 26
           ||||||||||||
Qy       4 TCAGCCACTGGA 15


RESULT   21
ID   US-08-397-470-23 STANDARD; DNA; UNC; 36 BP.
AC   xxxxxx
DT
DE   Sequence 23, Application US/08397470
CC   Sequence 23, Application US/08397470
CC   Patent No. 5652353
CC    GENERAL INFORMATION:
CC      APPLICANT:  Fiers, W.
CC      APPLICANT:  Tavernier, J.
CC      APPLICANT:  Van Ostade, X.
CC      TITLE OF INVENTION:  TNF-Muteins
CC      NUMBER OF SEQUENCES:  24
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Hoffmann-La Roche Inc.
CC        STREET:  340 Kingsland Street
CC        CITY:  Nutley
CC        STATE:  New Jersey
CC        COUNTRY:  USA
CC        ZIP:  07110
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, Version #1.25
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/397,470
CC        FILING DATE:  01-MAR-1995
CC        CLASSIFICATION:  435
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  US 07/794,400
CC        FILING DATE:  20-NOV-1991
CC        APPLICATION NUMBER:  EP 90810901.0
CC        FILING DATE:  21-NOV-1990
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Krovatin, William
CC        REGISTRATION NUMBER:  33256
CC        REFERENCE/DOCKET NUMBER:  4105/136-00
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  (201) 235-4387
CC        TELEFAX:  (201) 235-3500
CC    INFORMATION FOR SEQ ID NO:  23:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  36 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  single
CC        TOPOLOGY:  linear
CC      MOLECULE TYPE:  DNA (oligonucleotide)
CC      FEATURE:
CC        NAME/KEY:  misc_feature
CC        LOCATION:  1..36
CC        OTHER INFORMATION:  /function= "PCR primer for
CC        OTHER INFORMATION:  mutagenesis"
CC        OTHER INFORMATION:  /note= "PCR primer for mutagenesis which is
CC        OTHER INFORMATION:  complementary to positions 219-184 of Seq. ID No. 56523
CC        OTHER INFORMATION:  2 with mismatched bases at positions 7-9 and 11-12
SQ   SEQUENCE 36 BP; 5 A; 11 C; 10 G; 10 T; 0 OTHER.

  Query Match           46.2%;  Score 12;  DB 2;  Length 36;
  Best Local Similarity 100.0%;  Pred. No. 1.93e+02;
  Matches    12;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db      15 TCAGCCACTGGA 26
           ||||||||||||
Qy       4 TCAGCCACTGGA 15


RESULT   22
ID   US-07-794-400-22 STANDARD; DNA; UNC; 36 BP.
AC   xxxxxx
DT
DE   Sequence 22, Application US/07794400
CC   Sequence 22, Application US/07794400
CC   Patent No. 5422104
CC    GENERAL INFORMATION:
CC      APPLICANT:  Fiers, W.
CC      APPLICANT:  Tavernier, J.
CC      APPLICANT:  Van Ostade, X.
CC      TITLE OF INVENTION:  TNF-Muteins
CC      NUMBER OF SEQUENCES:  24
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Hoffmann-La Roche Inc.
CC        STREET:  340 Kingsland Street
CC        CITY:  Nutley
CC        STATE:  New Jersey
CC        COUNTRY:  USA
CC        ZIP:  07110
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, Version #1.25
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/07/794,400
CC        FILING DATE:  19911120
CC        CLASSIFICATION:  435
CC      PRIOR APPLICATION DATA:
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CC        APPLICATION NUMBER:  EP 90810901.0
CC        FILING DATE:  21-NOV-1990
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Krovatin, William
CC        REGISTRATION NUMBER:  33256
CC        REFERENCE/DOCKET NUMBER:  4105/136-00
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  (201) 235-4387
CC        TELEFAX:  (201) 235-3500
CC    INFORMATION FOR SEQ ID NO:  22:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  36 base pairs
CC        TYPE:  NUCLEIC ACID
CC        STRANDEDNESS:  single
CC        TOPOLOGY:  linear
CC      MOLECULE TYPE:  DNA (oligonucleotide)
CC      FEATURE:
CC        NAME/KEY:  misc_feature
CC        LOCATION:  1..36
CC        OTHER INFORMATION:  /function= "PCR primer"
CC        OTHER INFORMATION:  /product= "primer 21/M5"
CC        OTHER INFORMATION:  /note= "PCR primer which is complementary to
CC        OTHER INFORMATION:  positions 219-184 of Seq. ID No. 5422104 2 with mismatched
CC        OTHER INFORMATION:  residues at positions 10-12."
SQ   SEQUENCE 36 BP; 4 A; 15 C; 9 G; 8 T; 0 OTHER.

  Query Match           46.2%;  Score 12;  DB 1;  Length 36;
  Best Local Similarity 100.0%;  Pred. No. 1.93e+02;
  Matches    12;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db      15 TCAGCCACTGGA 26
           ||||||||||||
Qy       4 TCAGCCACTGGA 15


RESULT   23
ID   5256648-14 STANDARD; DNA; UNC; 42 BP.
AC   xxxxxx
DT   01-JAN-1900
DE   Patent No. 5256648.
CC  Patent No. 5256648
CC      APPLICANT: GASPARRO, FRANCIS P.;EDELSON,RICHARD L.
CC      TITLE OF INVENTION: SELECTIVE INHIBITION OF GENE EXPRESSION
CC  BY PHOTOACTIVATABLE OLIGONUCLEOTIDES
CC      NUMBER OF SEQUENCES: 40
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/07/410,622
CC        FILING DATE: 21-SEP-1989
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER: 299,265
CC        FILING DATE: 23-JAN-1989
CC        APPLICATION NUMBER: 146,571
CC        FILING DATE: 21-JAN-1988
CC  SEQ ID NO:14:
CC        LENGTH: 39
SQ   Sequence 42 BP; 10 A; 10 C; 9 G; 10 T; 3 other;

  Query Match           46.2%;  Score 12;  DB 5;  Length 39;
  Best Local Similarity 100.0%;  Pred. No. 1.93e+02;
  Matches    12;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db      25 CAGCCACTGGAT 36
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Qy       5 CAGCCACTGGAT 16


RESULT   24
ID   5256648-19 STANDARD; DNA; UNC; 42 BP.
AC   xxxxxx
DT   01-JAN-1900
DE   Patent No. 5256648.
CC  Patent No. 5256648
CC      APPLICANT: GASPARRO, FRANCIS P.;EDELSON,RICHARD L.
CC      TITLE OF INVENTION: SELECTIVE INHIBITION OF GENE EXPRESSION
CC  BY PHOTOACTIVATABLE OLIGONUCLEOTIDES
CC      NUMBER OF SEQUENCES: 40
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/07/410,622
CC        FILING DATE: 21-SEP-1989
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER: 299,265
CC        FILING DATE: 23-JAN-1989
CC        APPLICATION NUMBER: 146,571
CC        FILING DATE: 21-JAN-1988
CC  SEQ ID NO:19:
CC        LENGTH: 39
SQ   Sequence 42 BP; 11 A; 10 C; 7 G; 11 T; 3 other;

  Query Match           46.2%;  Score 12;  DB 5;  Length 39;
  Best Local Similarity 100.0%;  Pred. No. 1.93e+02;
  Matches    12;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db       8 CAGCCACTGGAT 19
           ||||||||||||
Qy       5 CAGCCACTGGAT 16


RESULT   25
ID   5256648-13 STANDARD; DNA; UNC; 42 BP.
AC   xxxxxx
DT   01-JAN-1900
DE   Patent No. 5256648.
CC  Patent No. 5256648
CC      APPLICANT: GASPARRO, FRANCIS P.;EDELSON,RICHARD L.
CC      TITLE OF INVENTION: SELECTIVE INHIBITION OF GENE EXPRESSION
CC  BY PHOTOACTIVATABLE OLIGONUCLEOTIDES
CC      NUMBER OF SEQUENCES: 40
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/07/410,622
CC        FILING DATE: 21-SEP-1989
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER: 299,265
CC        FILING DATE: 23-JAN-1989
CC        APPLICATION NUMBER: 146,571
CC        FILING DATE: 21-JAN-1988
CC  SEQ ID NO:13:
CC        LENGTH: 39
SQ   Sequence 42 BP; 11 A; 10 C; 7 G; 11 T; 3 other;

  Query Match           46.2%;  Score 12;  DB 5;  Length 39;
  Best Local Similarity 100.0%;  Pred. No. 1.93e+02;
  Matches    12;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db       8 CAGCCACTGGAT 19
           ||||||||||||
Qy       5 CAGCCACTGGAT 16


RESULT   26
ID   US-08-343-682-11 STANDARD; DNA; UNC; 49 BP.
AC   xxxxxx
DT
DE   Sequence 11, Application US/08343682
CC   Sequence 11, Application US/08343682
CC   Patent No. 5688511
CC    GENERAL INFORMATION:
CC      APPLICANT:  Gaynor, Richard B.
CC      APPLICANT:  Ou, S.-H. I.
CC      APPLICANT:  Wu, Foon K.
CC      TITLE OF INVENTION:  Cellular Protein TDP-43 and Regulation
CC      TITLE OF INVENTION:  of HIV-1 Gene Expression
CC      NUMBER OF SEQUENCES:  17
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Arnold, White & Durkee
CC        STREET:  P O. Box 4433
CC        CITY:  Houston
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CC        STATE:  TX
CC        COUNTRY:  US
CC        ZIP:  77210
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, Version #1.25
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/343,682
CC        FILING DATE:  22-NOV-1994
CC        CLASSIFICATION:  435
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Mayfield, Denise L.
CC        REGISTRATION NUMBER:  33,732
CC        REFERENCE/DOCKET NUMBER:  UTSD:355/MAY
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  713/787-1400
CC        TELEFAX:  713/789-2679
CC        TELEX:  N/A
CC    INFORMATION FOR SEQ ID NO:  11:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  49 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  single
CC        TOPOLOGY:  linear
CC      MOLECULE TYPE:  DNA (genomic)
SQ   SEQUENCE 49 BP; 9 A; 13 C; 12 G; 15 T; 0 OTHER.

  Query Match            46.2%;  Score 12;  DB 2;  Length 49;
  Best Local Similarity  77.3%;  Pred. No. 1.93e+02;
  Matches    17;  Conservative    0;  Mismatches   5;  Indels   0;  Gaps   0;

Db       7 CTCAGATGCTGCATATAAGCAG 28
           |||||   ||| || |||||||
Qy       3 CTCAGCCACTGGATTTAAGCAG 24


RESULT   27
ID   US-07-994-469A-26 STANDARD; DNA; UNC; 49 BP.
AC   xxxxxx
DT
DE   Sequence 26, Application US/07994469A
CC   Sequence 26, Application US/07994469A
CC   Patent No. 5519119
CC    GENERAL INFORMATION:
CC      APPLICANT:  Yamada, No. 5519119utoshi
CC      APPLICANT:  Kato, Masanari
CC      APPLICANT:  Miyata, Keizo
CC      APPLICANT:  Aoyama, Yoshiyuki
CC      APPLICANT:  Shikama, Hiroshi
CC      TITLE OF INVENTION:  Polypeptide
CC      NUMBER OF SEQUENCES:  101
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
CC        ADDRESSEE:  P.C.
CC        STREET:  1755 Jefferson Davis Highway, Fourth Floor
CC        CITY:  Arlington
CC        STATE:  Virginia
CC        ZIP:  22202
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, Version #1.25
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/07/994,469A
CC        FILING DATE:  21-DEC-1992
CC        CLASSIFICATION:  435
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Oblon, No. 5519119man F.
CC        REGISTRATION NUMBER:  24,618
CC        REFERENCE/DOCKET NUMBER:  72-085-0 FWC
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  (703)413-3000
CC        TELEFAX:  (703)413-2220
CC        TELEX:  248855 OPAT UR
CC    INFORMATION FOR SEQ ID NO:  26:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  49 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  unknown
CC        TOPOLOGY:  linear
CC      MOLECULE TYPE:  DNA (genomic)
SQ   SEQUENCE 49 BP; 9 A; 16 C; 16 G; 9 T; 0 OTHER.

  Query Match            46.2%;  Score 12;  DB 1;  Length 49;
  Best Local Similarity 100.0%;  Pred. No. 1.93e+02;
  Matches    12;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db       2 TCCAGTGGCTGA 13
           ||||||||||||
Cp      15 TCCAGTGGCTGA 4


RESULT   28
ID   PCT-US93-12388-486 STANDARD; DNA; UNC; 50 BP.
AC   xxxxxx
DT
DE   Sequence 486, Application PC/TUS9312388
CC   Sequence 486, Application PC/TUS9312388
CC    GENERAL INFORMATION:
CC      APPLICANT:
CC      TITLE OF INVENTION:  Sequence-Directed DNA Binding
CC      TITLE OF INVENTION:  Molecules, Compositions and Methods
CC      NUMBER OF SEQUENCES:  641
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Genelabs Technologies, Inc.
CC        STREET:  505 Penobscot Drive
CC        CITY:  Redwood City
CC        STATE:  CA
CC        COUNTRY:  USA
CC        ZIP:  94063
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, Version #1.25
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  PCT/US93/12388
CC        FILING DATE:
CC        CLASSIFICATION:
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  US 08/123,936
CC        FILING DATE:  17-SEP-1993
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  US 07/996,783
CC        FILING DATE:  23-DEC-1992
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Fabian, Gary R.
CC        REGISTRATION NUMBER:  33,875
CC        REFERENCE/DOCKET NUMBER:  4600-0175.41/G19PCT2
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  (415) 324-0880
CC        TELEFAX:  (415) 324-0960
CC    INFORMATION FOR SEQ ID NO:  486:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  50 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  single
CC        TOPOLOGY:  linear
CC      MOLECULE TYPE:  RNA (genomic)
CC      HYPOTHETICAL:  NO
CC      ORIGINAL SOURCE:
CC        INDIVIDUAL ISOLATE:  Human T-cell Lymphotropic virus type
CC        INDIVIDUAL ISOLATE:  III  (HIV-1)
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SQ   SEQUENCE 50 BP; 9 A; 14 C; 13 G; 14 T; 0 OTHER.

  Query Match           46.2%;  Score 12;  DB 4;  Length 50;
  Best Local Similarity  77.3%;  Pred. No. 1.93e+02;
  Matches   17;  Conservative    0;  Mismatches   5;  Indels   0;  Gaps   0;

Db       9 CTCAGATCCTGCATATAAGCAG 30
           |||||   ||| || |||||||
Qy       3 CTCAGCCACTGGATTTAAGCAG 24


RESULT   29
ID   US-08-171-389-487 STANDARD; DNA; UNC; 50 BP.
AC   xxxxxx
DT
DE   Sequence 487, Application US/08171389
CC   Sequence 487, Application US/08171389
CC   Patent No. 5578444
CC    GENERAL INFORMATION:
CC      APPLICANT:  Edwards, Cynthia A.
CC      APPLICANT:  Cantor, Charles R.
CC      APPLICANT:  Andrews, Beth M.
CC      APPLICANT:  Turin, Lisa M.
CC      APPLICANT:  Fry, Kirk E.
CC      TITLE OF INVENTION:  Sequence-Directed DNA Binding
CC      TITLE OF INVENTION:  Molecules, Compositions and Methods
CC      NUMBER OF SEQUENCES:  641
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Genelabs Technologies, Inc.
CC        STREET:  505 Penobscot Drive
CC        CITY:  Redwood City
CC        STATE:  CA
CC        COUNTRY:  USA
CC        ZIP:  94063
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, Version #1.25
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/171,389
CC        FILING DATE:
CC        CLASSIFICATION:  435
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  US 08/123,936
CC        FILING DATE:  17-SEP-1993
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  US 07/996,783
CC        FILING DATE:  23-DEC-1992
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  US 07/723,618
CC        FILING DATE:  27-JUN-1991
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  US 08/081,070
CC        FILING DATE:  22-JUN-1993
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Fabian, Gary R.
CC        REGISTRATION NUMBER:  33,875
CC        REFERENCE/DOCKET NUMBER:  4600-0175/G19P3
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  (415) 324-0880
CC        TELEFAX:  (415) 324-0960
CC     INFORMATION FOR SEQ ID NO:  487:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  50 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  single
CC        TOPOLOGY:  linear
CC      MOLECULE TYPE:  RNA (genomic)
CC      HYPOTHETICAL:  NO
CC      ORIGINAL SOURCE:
CC        INDIVIDUAL ISOLATE:  Aids-associated retrovirus
CC        INDIVIDUAL ISOLATE:  (arv-2;proviral)
SQ   SEQUENCE 50 BP; 8 A; 13 C; 13 G; 16 T; 0 OTHER.

  Query Match           46.2%;  Score 12;  DB 1;  Length 50;
  Best Local Similarity  77.3%;  Pred. No. 1.93e+02;
  Matches   17;  Conservative    0;  Mismatches   5;  Indels   0;  Gaps   0;

Db       9 CTCAGATGCTGCATATAAGCAG 30
           |||||   ||| || |||||||
Qy       3 CTCAGCCACTGGATTTAAGCAG 24


RESULT   30
ID   US-08-123-936-487 STANDARD; DNA; UNC; 50 BP.
AC   xxxxxx
DT
DE   Sequence 487, Application US/08123936
CC   Sequence 487, Application US/08123936
CC   Patent No. 5726014
CC    GENERAL INFORMATION:
CC      APPLICANT:  Edwards, Cynthia A.
CC      APPLICANT:  Cantor, Charles R.
CC      APPLICANT:  Andrews, Beth M.
CC      APPLICANT:  Turin, Lisa M.
CC      TITLE OF INVENTION:  Screening Assay for the Detection of
CC      TITLE OF INVENTION:  DNA-Binding Molecules
CC      NUMBER OF SEQUENCES:  640
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Genelabs Technologies, Inc.
CC        STREET:  505 Penobscot Drive
CC        CITY:  Redwood City
CC        STATE:  CA
CC        COUNTRY:  USA
CC        ZIP:  94063
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, Version #1.25
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/123,936
CC        FILING DATE:
CC        CLASSIFICATION:  435
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  US 07/996,783
CC        FILING DATE:  23-DEC-1992
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  US 07/723,618
CC        FILING DATE:  27-JUN-1991
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Fabian, Gary R.
CC        REGISTRATION NUMBER:  33,875
CC        REFERENCE/DOCKET NUMBER:  4600-0075.32/G19P2
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  (415) 324-0880
CC        TELEFAX:  (415) 324-0960
CC     INFORMATION FOR SEQ ID NO:  487:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  50 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  single
CC        TOPOLOGY:  linear
CC      MOLECULE TYPE:  RNA (genomic)
CC      HYPOTHETICAL:  NO
CC      ORIGINAL SOURCE:
CC        INDIVIDUAL ISOLATE:  Aids-associated retrovirus
CC        INDIVIDUAL ISOLATE:  (arv-2;proviral)
SQ   SEQUENCE 50 BP; 8 A; 13 C; 13 G; 16 T; 0 OTHER.

  Query Match           46.2%;  Score 12;  DB 2;  Length 50;
  Best Local Similarity  77.3%;  Pred. No. 1.93e+02;
  Matches   17;  Conservative    0;  Mismatches   5;  Indels   0;  Gaps   0;

Db       9 CTCAGATGCTGCATATAAGCAG 30
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              ||||||   ||| ||  |||||||
Qy        3 CTCAGCCACTGGATTTAAGCAG 24
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Search completed: Mon Aug 2 12:23:25 1999
Job time : 84 secs.